Sequence 17641, A Sequence 17641, A Sequence 4, Appl Sequence 694, Appl Sequence 694, Appl Sequence 111, Appl Sequence 111, Appl Sequence 77120, A Sequence 77121, A Sequence 1100, A Sequence 11001, Sequence 116411, Sequence 116411, Sequence 2255, Appl Sequence 240, Appl Sequence 11, Appl Sequence 11

6 US-10-027-632-38125 US-09-938-842A-694 US-09-938-842A-694 US-09-938-842A-694 US-09-938-842A-694 US-09-938-842A-694 US-09-938-842A-694 US-10-108-26A-1417 US-10-027-632-77120 US-10-027-632-77121 US-10-027-632-77121

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Sequence 30. Application US/10313994
; Sequence 30. Application US/10313994
; Publication No. US20030162718A1
; GENERAL INFORMATION:
; APPLICANT: Selected, Michael E.
; APPLICANT: Tang, Yi-Quan
; APPLICANT: Tang, Yi-Quan
; APPLICANT: Tang, Antimicrobial Theta Defensins and Methods of Using Same
; TITLE OF INVERTION: Antimicrobial Theta Defensins and Methods of Using Same
; TITLE OF INVERTION: Antimicrobial Theta Defensins and Methods of Using Same
; TITLE OF INVERTION: Autimicrobial Theta Defensins and Methods of Using Same
; TITLE OF INVERTION UNMERR: US/10/313,994
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: US/09/309,487
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 30
; EPROMETATION OF 2.0
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US-10-313-994-30
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                                                                                                                                                                                                                                                                            ; Search time 214 Seconds (without alignments) 3127.023 Million cell updates/sec
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3 US-10-027-632-77713

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10 US-10-004-860-97

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6 US-10-264-37-115

6 US-10-264-37-115

7 US-10-369-493-33481

US-09-897-576-863

1 US-10-037-192-1786

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                                       GenCore version
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PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 77713
LENGTH: 450
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1 Similarity 52.8%;
66; Conservative (
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Best Local Similarity
Matches 66; Conserv
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                                                                                                            ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-77713
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ORGANISM: Human
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                                                                                                                                                                  Sequence 31, Application US/10313994

publication No. US20030162718A1

GENERAL INFORMATION:

APPLICANT: Seleted, Michael E.

APPLICANT: Tang, Yi-Quan

APPLICANT: Yuan, Jun

APPLICANT: Yuan, Jun

APPLICANT: Yuan, Jun

TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same

FILE REFERENCE: PUC 3095

CURRENT PILING DATE: 2002-12-05

CURRENT FILING DATE: 2002-12-05

PRIOR FILING DATE: 1999-05-10

NUMBER OF SEQ ID NOS: 31

SEQ ID NO 31

LENGTH: 132
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| Sequence 77713, Application US/10027632
| Publication No. US20020198371A1
| GENERAL INFORMATION:
| APPLICANT: Wang, David G.
| TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
| TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
| TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
| TITLE OF INVENTION: IDENTION: POLYMORES: US/10/027,632
| CURRENT APPLICATION NUMBER: US 60/18,006
| PRIOR APPLICATION NUMBER: US 60/198,676
| PRIOR FILING DATE: 2000-07-12
| PRIOR APPLICATION NUMBER: US 60/193,483
| PRIOR FILING DATE: 2000-03-29
| PRIOR FILING DATE: 2000-03-29
| PRIOR FILING DATE: 2000-02-24
| PRIOR FILING DATE: 1999-11-23
| PRIOR FILING DATE: 1999-11-23
| PRIOR FILING DATE: 1999-09-28
| PRIOR FILING DATE: 1999-09-28
| PRIOR FILING DATE: 1999-09-28
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Best Local Similarity 90.0%;
Matches 117; Conservative (
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ORGANISM: Artificial Sequence
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Sequence 77131, Application US/10027632

Publication No. US20030204075A9

GENERAL INFORMATION:

Publication No. US20030204075A9

GENERAL INFORMATION:

TITLE OF INVENTION: IGentification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REPRESENCE: 108827.129

CURRENT APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2002-04-30

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-00-29

PRIOR PRIOR DATE: 2000-03-29

PRIOR PRIOR DATE: 2000-03-29

PRIOR PRIOR DATE: 2000-03-29

PRIOR PRIOR DATE: 2000-03-29

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-10-28

PRIOR PLING DATE: 1999-10-38

PRIOR PLING DATE: 1999-10-38
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23.2%; Score 30.6; DB 13; Length 450; 52.8%; Pred. No. 0.27;
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Pred. No. 0.27;
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PRIOR FILING DATE: 1997-06-06
PRIOR FILING DATE: 1997-06-06
PRIOR PILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,919
PRIOR PILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,919
PRIOR PILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,919
PRIOR PILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,999
PRIOR PILING DATE: 1997-06
                                                R FILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/048,880

R PILING DATE: 1997-06-06

R FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/068,064
FILING DATE: 1997-12-18
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      1997-06-06
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                                                                                                                               Sequence 4727, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
ITLLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AECOMICA---2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 4727
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OTHER INFORMATION: EXPRESED IN ADULT LIVER, SIGNAL = 0.71

OTHER INFORMATION: EXPRESED IN BALLA : SIGNAL = 1.7

OTHER INFORMATION: EXPRESED IN BTALL LIVER, SIGNAL = 3.5

OTHER INFORMATION: EST_HUMAN HIT: BG680371.1, EVALUE 0.00e+00

OTHER INFORMATION: ST. HUMAN HIT: G114782799, EVALUE 9.60e-01

OTHER INFORMATION: LST_HUMAN HIT: BG680371.1, EVALUE 0.00e+00

US-10-029-386-4727
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Fublication No US20030181692A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILLE REFERENCE: P2007P2
CURRENT APPLICATION NUMBER: US/09/933,767
CURRENT FILING DATE: 2001-08-22
FRIOR APPLICATION NUMBER: 60/184,836
FRIOR APPLICATION NUMBER: 60/184,836
FRIOR FILING DATE: 2000-02-24
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 1998-12-04
FRIOR FILING DATE: 1998-12-04
FRIOR FILING DATE: 1998-12-04
FRIOR FILING DATE: 1998-12-04
FRIOR FILING DATE: 1998-06-04
FRIOR FILING DATE: 1998-06-04
FRIOR APPLICATION NUMBER: 60/048,885
FRIOR APPLICATION NUMBER: 60/048,885
FRIOR APPLICATION NUMBER: 60/049,375
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Best Local Similarity 52.8
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Homo sapiens FEATURE:
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228 ATTTC 232
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                                                                              RESULT 5
US-10-029-386-4727
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                                                                                                                                                   Score 30.6; DB 13; Length 1985;
Pred. No. 0.46;
0; Mismatches 59; Indels 0;
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TITLE OF INVENTION: 207 Human Secreted Proteins TITLE OF INVENTION: 207 Human Secreted Proteins CURRENT PAPPLICATION NUMBER: US/10/023,282
CURRENT FILING DATE: 1098-12-04
EARLIER PILING DATE: 1998-06-105
EARLIER PILING DATE: 1998-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER PILING DATE: 199
; OTHER INFORMATION: n equals a,t,g, or c US-10-004-860-97
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ARLIER FILING DATE: 1997-06-06
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                                                                                                                                                              Query Match 23.2%;
Best Local Similarity 52.8%;
Matches 66; Conservative
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; Sequence 97, Application US/10004860
; Publication No. US20030065160A1
; GENERAL INFORMATION:
; TITLE OF INVENTION:
; TILE REFERENCE: PZ007P1
; CURRENT FAPLICATION NUMBER: US/10/004,860
; CURRENT FILION DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 97
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US-09-933-767-97
          PRIOR APPLICATION NUMBER: 60/068,053
PRIOR FILING DATE: 1997-12-18
PRIOR FILING DATE: 1997-12-18
PRIOR PEPLICATION NUMBER: 60/079,160
PRIOR PELLING DATE: 1998-01-30
PRIOR PELLING DATE: 1998-01-30
PRIOR FILING DATE: 1998-01-30
PRIOR FILING DATE: 1998-01-30
PRIOR FILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR FILING DATE: 1998-05-18
PRIOR FILING DATE: 1998-05-18
PRIOR PLING DATE: 1998-05-18
PRIOR FILING DATE: 1998-07-18
PRIOR FILING DATE: 1998-07-15
PRIOR FILING DATE: 1998-07-15
PRIOR FILING DATE: 1998-07-15
PRIOR FILING DATE: 1998-07-15
PRIOR FILING DATE: 1998-07-10
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Query Match 23.2%; Best Local Similarity 52.8%; Matches 66; Conservative

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RESULT 7 US-10-004-860-97

TYPE: DNA ORGANISM: Homo sapiens

FEATURE: NAME/KEY: SITE

SOFTWARE: Patentin Ver. 2. SEQ ID NO 97 LENGTH: 1985

TYPE: DNA ORGANISM: Homo sapiens

FEATURE:

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APPLICANT: Birse et al.
TITLE OF INVENTYON: Nucleic Acids, Proteins, and Antibodies
FILE REPERRNCE: PA11P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR PILING DATE: 2001-05-18
PRIOR PILING DATE: 2001-05-19
PRIOR PILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 115
LENGTH: 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (5). (5) OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
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                                EARLIER APPLICATION UNBER: 60/048,970
EARLIER FILING DATE: 1997-66-06
EARLIER PILING DATE: 1997-66-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1998-07-15
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LOCATION: (332)
OTHER INFORMATION: n equals a,t,g, or c
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ORGANISM: Homo sapiens
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0; Gaps

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Sequence 33481, Application US/10369493

Publication No. US20030233675A1

Publication No. US20030233675A1

Publication No. US20030233675A1

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Glater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: BEARESSION OF MICROBIAL PROFEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: USANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10 (52052)B

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 33481

LENTH: 2301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 22.9%; Score 30.2; DB 16; Best Local Similarity 56.6%; Pred. No. 0.69; Matches 56; Conservative 0; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA; OSGANISM: Desulfitobacterium hafniense US-10-369-493-33481
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1583 CCCAGTGTCTTCAGGTTTCCCAAGACCACTTCCCTGTGGGCTTCCAAAATGGCCTTTATC 1642

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RESULT 9
US-10-264-237-115
Sequence 115, Application US/10264237
Publication No. US20040009491A1
GENERAL INFORMATION:

4 CCTIGICIACTAGICCCTIACCGAGIAAGGAAAIGIACCGGACIITTIGCGGCGAGAAGGI

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Tue Oct 12 09:20:48 2004

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6033 TTCCTCACCGAGTTCAGAGATGCCCCAGGGTACTGCAGCATTCAGGGGAATGTCTTCTC 5974
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Publication No. US2020198371A1

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Telephymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TILE OF INVENTION: POLYMORPER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR PLING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR PLING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1000-02-24
PRIOR FILING DATE: 1000-02-24
PRIOR FILING DATE: 1000-02-11-23
PRIOR FILING DATE: 1000-02-24
PRIOR FILING DATE: 1000-02-34
                                                                                           48 TTTGCGCCGAGAAGTGAAAGTCTCAGTCGCTTTCCGAACTCCACGTAAACGTGTGCTCC
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                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                             US-10-087-192-1786/c

Sequence 1786, Application US/10087192

Sequence 1786, Application US/10087192

PUBLication No. US20020182586A1

GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: CANCER
TITLE OF INVENTION: UNWERE: US/10/087,192
CURRENT APPLICATION NUMBER: US 09/747,377

PRIOR PELING DATE: 2000-12-20

PRIOR PILING DATE: 2000-12-20

PRIOR FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 2059

SOFTWARRE: FARSEQ for Windows Version 4.0

SEQ ID NO 1786

LENGTH. 26.42
                              27; Indels
Best Local Similarity 62.0%; Pred. No. 7.5; Matches 44; Conservative 0; Mismatches
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APPLICATION NUMBER: US 60/156,358
BILING DATE: 1999-09-28
APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                                                                        3568 Trcrrcaccaa 3558
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Matches 56; Conser
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; Sequence 37892, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
; APPLICANT: Li Ping
; TILE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TILE REFERENCE: 38-21(53221)B
; CURRENT FILING DATE: 2003-05-14
; SEQ ID NOS: 204966
; SEQ ID NOS: 204966
; SEQ ID NOS: 24966
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                                                                                                                                                                                                                                                                          APPLICANT: Chang, H.
APPLICANT: Chang, H.
APPLICANT: Zhu, T.
APPLICANT: Zhu, T.
APPLICANT: Zhu, T.
APPLICANT: Wang, X.
APPLICANT: Wooper, Bret
TITLE OF INVENTION: Promoters for regulation of plant expression
FILE REFERENCE: 1360,00103.
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR PLIANG DATE: 2000-06-23
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 875
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 863
LENGTH...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 TCAGTCGCTTTCCGAACTCCACGTAAACGTGTGCT 105
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Pred. No. 5.6;
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                                                                                                                            Sequence 863, Application US/09887576
Patent No. US/2020144047A1
GENERAL INFORMATION:
APPLICANT: Brown, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 21.1%;
Best Local Similarity 55.8%;
Matches 53; Conservative (
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US-09-887-576-863
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ORGANISM: Oryza sativa
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US-10-437-963-37892/c
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UG-10-27-612-38125/c

Sequence 38125, Application US/10027632

Publication No. US2030204075A9

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 10827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US 60/18,006

PRIOR PILING DATE: 2000-04-30

PRIOR PILING DATE: 2000-04-20

PRIOR PELING DATE: 2000-04-20

PRIOR PILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-24

PRIOR PILING DATE: 2000-03-24

PRIOR FILING DATE: 1000-03-24

PRIOR FILING DATE: 1000-03-24

PRIOR PILING DATE: 1009-01-28

PRIOR PILING DATE: 1009-01-28

PRIOR PILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-08-08

NUMBER OF SEQ ID NOS: 325720

SOFTWARE FEATURE FEATURE WINDOW VERSION 4.0

SEQ ID NO 38125

LENGTH: 409
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                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                   Query Match 20.3%; Score 26.8; DB 13; Length 409; Best Local Similarity 55.3%; Pred. No. 7.8; Matches 52; Conservative 0; Mismatches 42; Indels 0;
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Pred. No. 7.8;
0; Mismatches 42; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 AAGTCTTTGTCTTTTCATGAACTCCGTTTAAATG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 AAGICICAGICGCTITCCGAACTCCACGIAAACG 99
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| PRIOR FILING DATE: 1999-08-09 | NUMBER OF SEQ ID NOS: 325720 | STORWARE: FastSEQ for Windows Version 4.0 | SEQ ID NO 38125 | LENGTH: 409 | TYPE: DNA | TYPE: DNA | TYPE: DNA | CRGANISM: Human | US-10-027-632-38125 |
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Best Local Similarity 55.3%;
Matches 52; Conservative (
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US-10-027-632-38125
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Search completed: October 11, 2004, 12:14:32 Job time : 217 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

October 11, 2004, 08:56:11; Search time 1398.5 Seconds (without alignments) 2818.597 Million cell updates/sec US-10-009-317A-30 132 1 ggaccttgtctactagtccc......cggcaaacaatattacagtg 132 IDENTITY NUC Gapop 10.0 , Gapext 1.0 Title: Perfect score: Sequence: Scoring table: Run on:

27513289 seqs, 14931090276 residues Searched:

55026578 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST:* Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	BF088574	BZ475082	CNS0150E
1	10	28	90
	23.3	23.3	23.3
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		193 10 BF088574	C 2 30.8 23.3 193 10 BF088574 BF0888 3 30.8 23.3 679 28 BZ475082 BZ4750

22058 RC3-GN0; 22068 RC3-GN0; 22060 RC3-GN0; 37927 QV0-DT0 7281 wk90£12; 3405 nn57h03;	17815 282044 29619 xe19h0 50166 xg36c0 20183 hv69b1 3092 tg25h01 74818 xy20f1	1089 wv874439 hrs	56048 ir37d19 5019 AUI-4811 5019 AUI-4811 504 AUI-4819 504 AUI-4819 504 AUI-4819 506 AUI-4819 506 AUI-4819 507 AUI-4819 508 602453 508 602453 508 602453	3376 UI-H-FL 6408 UI-H-PL 6408 UI-H-PL 738 wol3bo5. 8317 UI-H-FL 6177 UI-H-EZ 3104 UI-H-FL 7608 UI-H-FL 70371 6026.92 827 ALS22827
BI05205 BI05206 BI05206 AW93792 AI827281 AA593405 AW43976	AW2478 AW1296 AW1501 BE2201 AI39309 AW4748	AW07108 BF1974 BQ1300 AI93708 BM2725 BI7530	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3337 6407 7407 7400 7400 7400 7400 7400 740
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FEATURES

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

1 (Dases I to 193)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Rogai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carralho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.Y., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC1-HT0881-130
900-014-bl1&t3=2000-09-13&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 28
High quality sequence start: 28
High quality sequence story: 192. BF088574 130900-014-bll HT0881 Homo sapiens cDNA, mRNA sequence. BF088574 Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Shotgun sequencing of the human transcriptome with ORF expressed roc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) RESULT 2 BF088574/c DEFINITION SOURCE ORGANISM MEDLINE PUBMED REFERENCE ACCESSION VERSION KEYWORDS JOURNAL FEATURES TITLE COMMENT LOCUS

/db_xref="texon:9606"
/da_xeef="texon:9606"
/dev_crage="Adult"
/clone_lib="HT0881"
/note="Corgan: head_neck; Vector: puc18; Site_1: SmaI;
/note="Corgan: head_neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - indwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions." 679 bp DNA linear GSS 13-DEC-2002 BONBK72TF BO 1.6 2 KB tot Brassica oleracea genomic clone BONBK72, genomic survey sequence. Brassica oleracea Brassica oleracea Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica. 62 25 /clone lib="BO_1.6_2 KB tot" /note="Vector: pHOS1; Site 1: BstXI; 1.6-2 kb sheared total DNA inserted into pHOS1 using BstXI linkers" 111 Accreaetretreariatrearesaetraretrecraetraretrarearetre 3 ACCTIGICIACIAGICCCTTACCGAGIAAGGAAATGIACCGGACTITIGCGGCGAGAAGG Gaps ö Score 30.8; DB 28; Length 679; Pred. No. 13; 0; Mismatches 47; Indels 0 23.3%; Score 30.8; DB 10; Length 193; 55.7%; Pred. No. 8.3; Email: cdtown@tigr.org DNA is from a dcubled haploid provided by Tom Osborn. Class: sheared ends. . (bases I to 6/9) Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fras Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001) Other_GSSs: BONBK72TR Conteat: Chris Town 63 TGAAAGTCTCTCTCTCCGAACTCCACGTAAACGTGTGCTCCT 108 51 riccaachterecitéchierearreitearereaacteaceareir 6 Indels 9712 Medical Center Drive, Rockville, MD 20850, 47; organism="Brassica oleracea" 0; Mismatches /mol_type="genomic DNA" /strain="TO1000DH3" /db_xref="taxon:3712" /clone="BONBK72" Location/Qualifiers BZ475082.1 GI:26776627 23.3%; Conservative Tel: 301-838-3523 Fax: 301-838-0208 679. . Similarity 59; TIGR Query Match Best Local S Query Match Best Local DEFINITION SOURCE ORGANISM ACCESSION VERSION KEYWORDS JOURNAL COMMENT Matches AUTHORS RESULT 3 BZ475082 REFERENCE FEATURES TITLE ORIGIN d ò 0 63

15 TCCCACACTAATTTCAGAGACACAATCGGCTTTTGTGGCAGGAAGGTTAAATTTCGGATA 74 17 TCCCTTACCGAGTAAGGAAATGTACCGGACTTTTGCGGCGAGAAGGTGAAAGTCTCAGTC 76 Gaps 0 Conservative 59; Matches

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Similarity

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Para: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
Project: This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-GN0268-170101-012-h08&t2=2001-01-7ft4=1)
Seq primer: puc 18 forward
High quality sequence start: 6
High quality sequence start: 6
High quality sequence stop: 320.
                                                                                                                                                                                                            Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                       Shotgun sequencing of the human transcriptome with ORF expressed
                                                          sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
   O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F.,
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/organism="Homo sapiens"
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACN14804 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL105776.1 GI:5618284
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Homo sapiens
Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Butheria, Primates, Catarrhini, Hominidae, Homo.

(bases 1 to 320)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagasi, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
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Neoptera; Endopterygota; Diptera; Erachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1007)
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/note==end : T7"
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ive 30; Mismatches
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Drosophila melanogaster
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de Souza, S.J. and

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/unl_type="maxNa"

/ub_xref="taxon:9606"

/dov_stage="Adult"

/dov_stage="Adult"

/dov_stage="Adult"

/dov_stage="Samis"

/note="Organ: placenta_normal; Vector: puc18; Site 1:

/note="Organ: placenta_normal; Vector: placenta_normal; Adult Normal; Institute for Cancer Research) profiles into the puc18 vector: Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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1 (bases 1 to 348)

1 bias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Slmpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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RC3-GN0268-170101-012-d09 GN0268 Homo sapiens cDNA, mRNA sequence.
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Homo sapiens
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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases I to 402)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Solasi, M.A., da Silva, W. Jr., Sago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deolitvèira, P.S., Bucher, P., Jongeneel, C.V., O'Here, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-GN0268-170101-012-a07&t3=2001-01-17&t4=1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   \operatorname{Simpson}, A \cdot J \cdot Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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52.8%; Pred. No. 12;
ive 0; Mismatches
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High quality sequence start: 51
High quality sequence stop: 365
                                                                                                                                                                                                                                                                            Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases 1 to 355)
1 (Bases 1 to 555)
Dias Neto.; Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., O'Hare,M.J., Goares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Singon, A.J.
Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Singon, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                                                                                   This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL futp://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-GN0268-170101-012-d09&t3=2001-01-17&t4=1)
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                                                                                                                                                                                                                   Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Shotgun sequencing of the human transcriptome with ORF expressed
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/organism="Homo sapiens"
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High quality sequence stop: 348.
                                                                                                                                                                Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
                                                                                                                                                                                                                                                                                                                                                   Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
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/mol_type="mRNA"

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/db_rzref="txxon:9606"

/dev_stage="Adult"

/clone_lib="bT0047"

/clone_lib="DT0047"

/note="Organ: denis drash; Vector: pucl8; Site_1: Smal;
Site_2: Smal; A min-library was made by cloning products
derived from ORSTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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1 (bases 1 to 4.0.

1 NCI-CGAP http://www.ncbi.nlm.nih.gov/nciegap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

1 Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapberfemail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                       Tel: +55-11-2704922
Fax: +55-11-2707001
Enabl: asimpson@ludwig.org.br
This sequence was defined from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=GVO-DT0047-170
200-122-hl22t3=2000-02-17&t4=1)
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High quality sequence start: 20
High quality sequence stop: 402.
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                                        Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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/dev stage="adult"
/lab_host="ntl0B (phage-resistant)"
/lab_host="ntl0B (phage-resistant)"
/clone_lib="NCI CGAP_Lib"
/note="Grgan: ling; Vector: pT7T3D-pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and Cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Scares and M. Patima Bonaldo. "
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nn57h03.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1088021 3',
AAS93405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: capbbs-remail.ih.gov

Email: capbbs-remail.ih.gov

Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Stratagene, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCT-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
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(Dases 1 to 451)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP); Tumor Gene Index

Unpublished (1997)
                                                                                                                                                                    1. 431
/organism="Homo sapiens"
/mol_type="mRNA"
/db refe="txxxn:9606"
/clone="IMAGE:2422703"
/tissue_type="squamous cell carcinoma, poorly
differentiated (4 pooled tumors, including primary and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 CCTTGTCTACTAGTCCCTTACCGAGTAAGGAAATGTACCGGAACTTTTGCGGCGAGAAGGT
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0
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52.8%; Pred. No. 13;
live 0; Mismatches 59; Indels 0
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 916 Std Error: 0.00
                                                                            Seg primer: -40UP from Gibco
High quality sequence stop: 413.
Location/Qualifiers
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nes 66; Conservative
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Clone distribution: NCI-CGAP clone distribution information

63

ORIGIN

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Email: cgapbs-remail.nih.gy

Fissue Procurement: DCTD/DTP CDNA Library Preparation: Ling

Fissue Procurement: DCTD/DTP CDNA Library Preparation: Ling

Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LLNI) DNA Sequencing by: Berkeley MGC sequencing

project Clone distribution: MGC clone distribution information can

be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bpry/image/image.html Base Calling / Quality

Scores: PHRED from University of Washingtion Genome Center. Vector

Trimming: cross match from University of Washingtion Genome Center.

PHRAP suite. Poly-T identification: patMatch.pl from Berkeley

Drosophila Genome Project. University of Mashingtion Genome Center:

http://www.genome.washington.edu Polyadenylation: Based upon the

presence of a Xhol site followed by a run of 14 or more T residues

at the beginning of the sequence, this CDNA insert was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2820449.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820449 3', AW247815
                  /clone lib="NCI_CGAP_Ut2"
/note="Organ: uterus; Vector: pCWV-SPORT6; Site_1: Sall;
/note="Organ: uterus; Vector: pCWV-SPORT6; Site_1: Sall;
ste_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"
                                                                                                                                                                                                                                                                                                                                             436 certeacteceágeacetraceceáacagarabagergaarecerregerergaarar 377
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (WGC)
Other ESTs: 2820449.Sprime
Contact: Robert Strausberg, Ph.D.
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/tissue type="small cell carcinoma"
/cell line="MGC3"
/lab host="MH10B (phage-resistant)"
/lab host="NIH MGC 7"
/clone lib="NIH MGC 7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: BCORI; CDNA made by oliqo-dT priming. Directionally cloned into ECORI/XhoI sites using the following 5'
                                                                                                                                                                                                                                                                                                4 CCTTGTCTACTAGTCCCTTACCGAGTAAGGAAATGTACCGGACTTTTGCGGCGAGAAGGT
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                                                                                                                                                                                                  Length 453;
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52.8%; Pred. No. 13;
cive 0; Mismatches
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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High quality sequence stop: 326.
Location/Qualifiers
'lab host="DH10B"
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Matches
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AW247815/c
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TITLE
JOURNAL
COMMENT
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Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmeirt Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image.image.html

Seq primer: -40UP from Gibco

High quality sequence stop: 418.
                                                                                                                                                                                                                          AW439761 LCGAP_Ut2 Homo sapiens cDNA clone IMAGE:2889206 3',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (base 1 to 453)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 CCTTGTCTACTAGTCCCTTACCGAGTAAGGAAATGTACCGGACTTTTGCGGCGAGAAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59; Indels
     Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 405.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.2%; Score 30.6; DE ilarity 52.8%; Pred. No. 13; Conservative 0; Mismatches
                                                                                                        /organism="Homo sapiens"
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                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1088021"
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                                                                                                                                                                                                             /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
                                                                                1. .451
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AW439761
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Best Local Similarity
Matches 66; Conserv
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AW439761/c
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467 bp mRNA linear EST 25-OCT-1999

AND ARABY OF THE MAGE: 2607615 3',
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/clone_lib="NCI_CGAP_Ut4"
//clone_lib="NCI_CGAP_Ut4"
//note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sal1;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.48 kb. Life Technologies catalog #:
11542-016"
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adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDAR synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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/db_xref="taxon:9606"
/clone="lMAGE:2607615"
/closue Lype="serous papillary carcinoma, high grade, pooled tumors"
                                                                                                                                                         4 CCTTGTCTACTAGTCCCTTACCGAGTAAGGAAATGTACCGGACTTTTGCGGCGAGAGGT
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Best Local Similarity 52.8%; Pred. No. 13;
Matches 66; Conservative 0; Mismatches 59;
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Best Local Similarity 52.8%; Pred. No. 13;
Matches 66; Conservative 0; Mismatches
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Contact: Sobert Strausberg, Ph.D.
Email: gapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llni.gov/bbrp//amage/image.html

Seq primer: -40UP from Gibco

High quality sequence stop: 416.
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3436604 XI NCI_CGAP_Utl Homo sapiens CDNA clone IMAGE:2629638 3',
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adenocarcinoma, 7 pooled tumors"
/lab host="NCI_CGAP_Utl"
/clone_lib="NCI_CGAP_Utl"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Life Technologies catalog #:
11538-014"
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                          435 CCTTCACTCCCCAGCACTTGCCCAACAGGATAAGCTGGATCCCCTTGGCCTTTTGAATAT 376
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I (bases 1 to 46).
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
CCTTGTCTACTAGTCCCTTACCGAGTAAGGAAATGTACCGGACTTTTGCGGCGAGAAGGT
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    .467
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/db_xref="taxon:9606"
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Tunor Gene Index
Institute, Cancer Sement Figure, Contact: Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-romail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Email: cgapbs-romail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., CDNA Library Preparation: M. Bento Scares, Ph.D.
CDNA Library Preparation: M. Bento Scares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Mashington University Genme Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 468.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="carcinoid"
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/clone_lb="NCI CGAP_Lu24"
/note="Organ: lung; Vector: pT7F3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP_LuS was prepared, and ss circles were made in vir.o. Following HAP purification, this DNA was used as tracer in a subtractive hybridization, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 144920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Patima Bonaldo. "
                                                BE220183 468 bp mRNA linear EST 03-JUL-2000 hv69bl0.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3178651 3',
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1 (bases 1 to 46).
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IVAGE:3178651"
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Search completed: October 11, 2004, 10:55:04 Job time : 1403.5 secs

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October 11, 2004, 08:25:36; Search time 1124.5 Seconds (without alignments) 5087.844 Million cell updates/sec
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132
1 ggacctcgtctactagtccc......cggttgacaatatttccgca 132
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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1: gb_ba:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequer Sequer Sequer Sequer	AC107644 Mus muscu	Mus musc Rattus n	AC119848 MUS MUSCU AL589766 MOUSE DNA BX248984 MOUSE DNA	AC119542 Mus muscu AC118868 Rattus no AC099298 Rattus no	Ephe Mus	AP000066 Homo sapi AP006291 Homo sapi	Нопо	Homo	Mou Pseu	AY113357 Drosophil AC014471 Drosophil	AC009462 Drosophil AC006495 Drosophil	AC009394 Drosophil	AL050399 Arabidops	AL161532 Arabidops AE007053 Mycobacte	AX704274 Sequence	AC087702 Trypanoso AC015938 Homo sapi	AC025882 Homo sapi	Mycoba	Mus musc	Highly	ношо sap Ношо sap		linear PAT 20-APR-2002			Ouellette,A.J. Lods of using same
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AL844144.10 GI:30842726
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Antimicrobial theta defensins and methods of using same
Patent: WO 0068265-A 31 16-NOV-2000;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)
Location/Qualifiers
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100.0%; Pred. No. 4.4e-34;
live 0; Mismatches 0;
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Sequence 30 from patent US 6335318.
AR181804 1 GI:20224018
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Sequence 31 from Patent W00068265.
AX047117
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AL844144 178965 bp DNA linear ROD 16-MAY-2003 Mouse DNA sequence from clone RP23-204D17 on chromosome 2, complete sequence.
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Antimicrobial theta defensins and methods of using same
Patent: WO 0068265-A.3 olf-NOV-2000;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)
Location/Qualifiers
Selsted,M.E., Tang,Y.-Q., Yuan,J. and Ouellette,A.J.
Antimicrobial Inhera defensins and methods of using same
Patent: US 6335118-A 30 01-JAN-2002;
Location/Qualifiers
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Best Local Similarity 90.0%;
Matches 117; Conservative (
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Best Local Similarity 90.0%;
Matches 117; Conservative
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us-10-009-317a-31.rge

SOURCE ORGANISM

KEYWORDS

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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Direct Submission

Direct Submission

Research, 320 Charles Street, Cambridge, MA 02141, USA

CE 3 (bases 1 to 241189)

Birren B., Wusbaum, C. inader, E., Abouelleil, A., Allen, N.,

Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,

Boyuslavkiy, L., Boukhgalter, B., Canarata, J., Chang, J., Choepel, Y.,

Collymore, A., Cook, A., Cook, P., Corum, B., Dakrellano, K.,

Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,

Ferreira, P., FitzGerald, M., Gage, D., Gadagan, J., Gardine, R.,

Ramat, A., Karatas, A., Kalls, C., Landers, T., Lerine, R.,

Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., Maclean, C.,

Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,

Madyen, C., Micol, K., Whova, T., Comnor, T., O'Donnell, P.,

O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,

Ramasany, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,

Roman, J., Schauer, S., Schubsack, R., Severy, P., Smith, C.,

Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubs, M.,

Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,

Vassiliev, H., Venkataraman, V. S., Wiel, R., Vo, A., Wilson, B., Wu, X.,

Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Research, 320 Charles Street, Cambridge, MA 02141, USA

On May 2, 2003 this sequence version replaced gi:22381169.

All repeats were identified using RepeatMasker:

All Research, S. A. R. S. Charles Street, Cambridge, Ma, D.,

Man, P., M.,

Man, M., M., M., M., M., M., M.,

Man, M., M., M., M., M., M., M.,

Mitcheats were identified using RepeatMasker:

All repeats were identified using RepeatMasker:

All Research, 320 Charles Street, Cambridge, M.,

All repeats were identified using RepeatMasker:
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Birren, B., Nusbaum, C. and Lander, E.
Mus musculus, clone RP23-55K6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://ftp.genome.washington.edu/RM/RepeatMasker.html
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                              FULLTOP, HTGS_ACTIVEFIN.
                                                                                                                   Mus musculus (house mouse)
                                     AC107644.4 GI:30315786
HTG; HTGS_PHASE2; HTGS_F
                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 241189)
ACCESSION
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made too resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL: Sw: SMISSROT; Tr:, TREMBL; Wp:, WORNPEP; Information on the WORNPEP database can be found at from the Rec1-23 Mouse BAC Library constructed by the group of Pieter de Jong.

From the REC1-23 Mouse BAC Library constructed by the group of Pieter de Jong.

VECTOR: PAGES ACCAPACE ACCAPAC
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                                                                                                                                                                                                                                               Direct Submission
Submitted (16-MAY-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, GB10 15A, UK. E-mail enquisities:
Cambridgeshire, GB10 15A, UK. E-mail enquisities:
On May 17, 2003 this sequence version replaced gii30140518.
Sequence from the Mouse Genome Sequencing Consortium whole genome shotgum may have been used to confirm this sequence. Sequence data from the whole genome shotgum alone has only been used where it has a phred quality of at least 30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 TCTACTAGTCCCTTACCGAGTAAGGAAATGTGCCGGACTTTTGCGGCGAGAGGCGAAAG 68
                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC107644 24.1189 bp DNA linear HTG 02-MAY-20
Mus musculus clone RP23-55K6, *** SEQUENCING IN PROGRESS ***, 14
ordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117188 reredaceaereaecaaecaaecaaecaaerarere 117154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /chromosome="2"
/clone="RP23-204D17"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .178965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---- Genome Center
                                     Mus musculus (house mouse)
                                                                                                                                                                                          (bases 1 to 178965)
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Best Local Similarity 58.9%;
Matches 56; Conservative (
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FEATURES

ORIGIN

g à RESULT 6 AC107644/C LOCUS DEFINITION

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Prediction of the coding sequences of mouse homologues of KIAA gene: III. the complete nucleotide sequences of 500 mouse KIAA-homologous cDNAs identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries
                                                                                                                                                                                                                                                                                                            Submitted (23-JUL-2003) Hisashi Koga, Kazusa DNA Research Institute, Laboratory for Genome Informatics; 2-6-7 Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan The CREATE program supported by Japan science and technology corporation; CDNA full insert sequencing: Kazusa DNA Research Institute; CDNA library construction, clone selection and 5'- & Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <258. .2834
/gene="mxIAA3015"
/gene="mxIAA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="PNPPEIAGAAGADGGAPVAEEQLSGERVRYPANDKIEDINGCP
KNRSQMIENIDACLAFLAAKGINYOGLSAEETRNGWLKAILGLFFSLSRYKQQQQQQQ
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VEMQSSASSKDSSOGXIIRFTLGQKKISRLPQPTARVAAGSBAKTRGGSAANNRRS
OSFNNYDKSKPVTSPPPAPPSNHEKEPLASSASSHPGMSENVPAPLENSPSVPWNCS
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EKLKLFNSKGGSKAGEGSASRDISCERLEIILPSFEETEELEATANRALSTVGPASSSP
KIALKGIAQRIFSRALTNKKSSPKGNEKEKEKQQREKEKEKEKEKGKDLTKRVSVTDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVTHSTLETTPDTNVTTELSGRSILSLTGRPTPLSWRLGQSSPRLQAGDAPSWGNGYP
PRANASRFISAEAGRYVYSAPLRRQLASRGSSICHVDVSDKADDDVDLEGISMDAPGY
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DR."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC120854 1near HTG 09-MAR-2003 Mus musculus clone RP23-32986, WORKING DRAFT SEQUENCE, 12 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSI SSQTVSGSVGTTQTTGSNTVSVQLPQPQQQYNHPNTATVAPFLYRSQTDTEGNVT
AESSSAGVSMEPSHYTKSGQPALEELTEDPEARRLRTVKNI ADLRQNLEETMSSLRGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLKEETKADLSGVAVTEMPKKSSKIASFIPKGGKLNSTKKEATAPSHSGIPKPGMKN
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                                                                                                                                                                                                                         2 (bases 1 to 5339)
Okazaki,N., Kikuno,R., Nagase,T., Ohara,O. and Koga,H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3167 TAACAGTCAAAACAGCAACCAAACCGCTCAAGCCCGAACCCTTG 3124
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/product="mkThA3015 protein"
/protein_id="BAC98290.1"
/db_xref="GI:37360624"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="adult"
/note="vector:modified pBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.0%; Score 30.4; D
55.8%; Pred. No. 35;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .5339
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="mbg13024"
                                                                                                                                DNA Res. 10 (4), 167-180 (2003)
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Matches
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AC120854
LOCUS
DEFINITION
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                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
JOURNAL
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PUBMED
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         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
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Saga,Y., Nagase,T., Ohara,O. and Koga,H.
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Mus musculus
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                         * This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 2836 2535: gap of 100 bp

* 25374 25473: contrig of 22438 bp in length

* 25474 28148: contrig of 2675 bp in length

* 28249 44862: contrig of 100 bp

* 4963 49959: contrig of 1664 bp in length

* 44963 49959: contrig of 4997 bp in length

* 49963 9959: contrig of 4997 bp in length
                                       NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8: gap of 100 bp
9: contig of 26261 bp in length
9: gap of 100 bp
1: contig of 3568 bp in length
9: gap of 100 bp
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contig of 10764 bp in length
gap of 100 bp
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of 13997 bp in length
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/db_xzef="kaxon:10090"
/clone="RP23-55K6"
/clone_lib="RPCI-23 Female Mouse BAC"
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Pred. No. 9.3;
0; Mismatches 39;
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    .241189
    /organism="Mus musculus'

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gap of 100
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larity 58.9%;
Conservative (
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Best Local Similarity
Matches 56; Conserv
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                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 207736)
Birren, B.; Nusbaum, C. and Lander, E.
Mus musculus, clone RP23-329B6
Unpublished
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Center: Whitehead Institute/ MIT Center for Genome Research
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Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
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                                     AC120854
AC120854.3 GI:28893742
HTG; HTGS_PHASE1; HTGS_DRAFT.
Mus musculus (house mouse)
Mus musculus
                                 ACCESSION
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COMMENT

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NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Sequencing vector: Plasmid, n/a; 100% of reads Sequencing vector: Plasmid, n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 204630 bases at least Q40 Consensus quality: 205639 bases at least Q30 Consensus quality: 205639 bases at least Q30 Insert size: 199000; agarose-fp Insert size: 206636; sum-of-contigs Quality coverage: 8.2 in Q20 bases; sum-of-contigs Quality coverage: 7.9 in Q20 bases; sum-of-contigs
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Marxy, D. Marie, Metrker, M. Lee, Abramzon, S., Addams, C., Alder, J., Alshrocks, S., Andi, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Aydedei, M., Baca, E., Baden, H., Balawi, V., Aoyagi, A., Aydedei, M., Barastead, M., Benahmed, F., Bladwin, D., Bandaranaike, D., Barber, M., Barrstead, M., Benahmed, F., Baldwin, D., Balar, J., Blark, C., Ederen, E., Carderon, E., Carderon, C., Carter, K., Cavazos, I., Cesar, H., Center, A., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chen, G., Chen, R., Chen, R., Chen, R., Diroh, H., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davis, C., Davy-Carroll, L., Poster, F., Fernandez, S., Filley, M., Flaggy, N., Probes, L., Poster, M., Ganza, L., Gante, R., Garcia, A., Garcia, A., Garcia, A., Garcia, A., Garcia, A., Garcia, A., Garcia, P., Garcia, P., Garcia, A., Garcia, A., Garcia, A., Garcia, A., Haves, M., Hans, G., Hawels, C., Hamilton, C., Hamilton, K., Harrey, Y., Havlak, P., Hule, M., Hamilton, C., Hamilton, K., Harrey, Y., Kaly, S., Hulyk, S., Hule, J., India, J., India, M., Mahlos, M., Mahlos, K., Martin, R., Martin, R
                                                                                                                                                                                                                                                                                              Rattus norvegicus clone CH230-296E17, *** SEQUENCING IN PROGRESS AC123263
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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                                                                                                                  DB 2; Length 207736;
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                                                                                                                  ch 23.0%; Score 30.4; DB 2; Length 20 1 Similarity 55.8%; Pred. No. 52; 58; Conservative 0; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                75 TCGCTCTCCGAACTCCACGGAAACGTCTGCTCCTCAAACGGTTG 118
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Rattus norvegicus (Norway rat)
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ON Sep 14, 2002 this sequence version replaced gi:21671637.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
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NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (29-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 216422) Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,O., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wheczyk,R., Wooden,H., Worley,K., Wight,D., Wright,D., Yan,J., Yaen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhao,S., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.
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Contact: hgsc-help@bcm.tmc.edu
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Unpublished
2 (bases 1 to 216422)
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Direct Submission
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Direct Submission

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Bursett Submission

Sesarch, 320 Charles Street, Cambridge, MA 02141, USA

Esesarch, 320 Charles Street, Cambridge, MA 02141, USA

Estable Street, Cambridge, MA 02141, USA

Birran, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,

Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,

Boyuslawikiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,

Collymore, A., Cook, P., Coram, B., DeArellano, K.,

Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,

Ferreira, P., Filzderald, M., Gage, D., Galagan, J., Gardyna, S.,

Graham, L., Grand-Pierre, N., Hafez, N., Hagoplan, D., Hagos, B.,

Hall, J., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C.,

Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,

Indblad-Toh, K., Liu, G., Lul, X., Mabbitt, R., Maclean, C.,

Macdonald, P., Major, J., Manning, J., Marthews, C., McCarthy, M.,

Neidrim, J., Menneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J.,

Nowei, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,

Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,

Roman, J., Schupack, R., Seaman, S., Severy, P., Smith, C.,

Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,

Vassiliev, H., Verkataraman, V. S., Viel, R., Vol, A., Wilson, B.,

Nyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.,

P., Faring, S., Paring, S., Maring, S., Well, R., Wall, R., Wall, R., Wall, R.,

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Jamas, J., Tesfaye, S., Theodore, J., Topham, K., Talvers, M.,

P., Wall, R., Wall, 
                                                                                                                                                                                                                                                  Direct Submission

Number Control Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

(Cases I to 239227)

Birren, B., Musbaum, C., Lander, E., Abouelleil, A., Allen, N.,

Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,

Bodyslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,

Collymore, A., Cook, A., Cooke, P., Corum, B., Dehrellano, K.,

Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,

Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gard-Pierre, N.,

Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,

Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,

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Mcdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,

Macdonald, P., Major, J., Peterson, K., Phunkhang, P., Pierre, N.,

Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,

Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C.,

Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,

Vassiliev, H., Venkattaman, V.S., Viel, R., Volaner, A. and Zody, M.

Direct Submission.
Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.wahington.edu/RM/RepeatMasker.html
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Web site: http://www-seq.wi.mit.edu
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Direct Submission
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Direct Submission
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JOURNAL
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                             109188 GGTAACGTGCTCTACCGTGGTGCTGATTAGCCTCCACTGTCTGGCCCCTCCTGAGCCCCA 109247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ROD 30-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I. (bases I to 239297)
Birren, B., Nusbaum, C. and Lander, E. Mus musculus chromosome 7, clone RP23-73B20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (02-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (bases 1 to 239297)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC119848 239297 bp DNA linear ROD 30-SEP-:
Mus musculus chromosome 7, clone RP23-73B20, complete sequence.
                                                                                                                                                                                                                                                                                                             32 GGAAATGTGCCGGACTTTTGCGGCGAGAAGGCGAAAGTCTCAGTCGCTCTCCGAACTCCA
                                                                                                                                              Match 23.0%; Score 30.4; DB 2; Length 216422; Local Similarity 59.1%; Pred. No. 52; conservative 0; Mismatches 36; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109248 CAGTGAGGCTCCTACACCAGTTGA 109275
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AC119848.8 GI:33438673
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           misc_feature
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VERSION
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TITLE
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AUTHORS
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AUTHORS
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SOURCE
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Direct Submission

Submitted (104-ARR-2002) Wellcome Trust Sanger Institute, Hinxton, cambridgeshier, CBN 15A, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
nn Dec 6, 2001 this sequence wersion replaced as il.6944103.

During sequence assembly data is compared from overlapping clone as variations
together with a note of the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one Mil subclone; and the
assembly was confirmed by resolved all sequencing and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em; EMBL; Sw;
SWISSROT; Tr:, TREMBL; Wp;, WORMPEP; Information on the WORMPEP
                                                                                                                                                                112020 ACTTGAGTAATGAGAGGAAGTGAGGCAGGTCCCTGGGGCCCTGCAGGAGAGAGTCGGAG 111961
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                                                                                                              74
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBACe3.6.
                                                                                                              15 AGTCCCTTACCGAGTAAGGAAATGTGCCGGACTTTTGCCGCCGAGAAGTCTCAG
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Length 239297;
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                                                          46; Indels
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     DB 10;
  23.0%; Score 30.4; D
55.8%; Pred. No. 53;
cive 0; Mismatches
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1 Similarity 58.2%; Pred. No. 59,
53; Conservative 0; Mismatches
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/clone="RP23-1964"
/clone="RP23-1964"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
Mus musculus
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Best Local Similarity
                                Local Similarity
nes 58; Conserv
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           Query Match
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us-10-009-317a-31.rge

DEFINITION

BX248984

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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CB Birren, B. Musbaum, C. Lander, B., Ali, A., Allen, N., Anderson, S., Birren, B., Musbaum, C., Lander, B., Ali, A., Allen, N., Anderson, S., Barrana, M., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Cooke, P., Daknellano, K., Dewar, K., Collymore, A., Cooke, P., Daknellano, K., Daknellano, E., Dadagan, J., Garata, P., Eltzderald, M., Gage, D., Galagan, J., Barten, M., Bloom, T., Barten, N., Hagos, B., Horton, L., Hulme, W., Iltev, I., Johnson, R., Jones, C., Kamat, A., Kalls, C., Landers, T., Lindelad, Toh, K., Murphy, T., Naylor, J., Nameus, L., Matora, J., Matchews, C., McCantthy, M., Meldrim, J., Moneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nameus, L., Mihova, T., Mathews, C., Norman, C. Horcon, T., Saymond, C., Retak, R., Rise, C., Roove, P., Roman, J., Roy, A., Saluber, S., Schupback, R., Seaman, S., Severy, P., Somen, J., Roy, A., Saymond, C., Retak, R., Rise, C., Roove, P., Roman, J., Roy, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Lender, B., State, Cambridge, M. Olliver, W. Vassiliev, H., Viel, R., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Lander, S., Cook, A., Wilson, B., Why, X., Myman, D., Young, G., Zainoun, J., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Elokey, S., Ferreira, P., Submitted (19-14807).

Sainten, B., Musbaum, C., Lander, B., Abouelleil, A., Allen, M., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Collymore, A., Cook, A., Wilson, B., Dartsis, L., Erickson, J., Fatcherald, M., Gage, D., Galagan, J., Changes, C., Claymore, J., Fatcherald, M., Gage, D., Galagan, J., Mandala, M., Maratas, A., Kalis, C., Mandala, P., Major, J., Manning, J., Matchew, C., McCarthy, M., Major, J., Manning, J., Matchew, C., McCarthy, M., Major, J., Manning, J., Matchew, C., McCarthy, M., Resilve, M., Retak, J., Peterson, K., Phurkhang, P., Pitchery, M., Peterson, K., Phurkhang, P., Radhupka, J., Peterson, K., P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases I to 194807)
Birren, B., Nusbaum, C. and Lander, E. Mus musculus chromosome 1, clone RP23-249L15
41372 TAGTTATCTGTCACTGAATAAGGAATTATACCAGATTTTAGCAGCATCATGCAGAAACAC 41431
                                                                                                                                                                                                                                                                                                                 AC129542 194807 bp DNA linear ROD 26-SEP-2003
Mus musculus chromosome 1, clone RP23-249L15, complete sequence.
AC129542
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                                                                                                                                             41432 TTAGTATCTACCAGTCTTAAATTTC 41462
                                                                              71 TCAGTCGCTCTCCGAACTCCACGGAAACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
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AC129542
LOCUS
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such one plasmid subclone or more than one M13 subclone; and the assembly was continued by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with thair source databases:

Em: FNBL; Sw: SMISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at from the RPG1-23 Mouse BAC Library constructed by the group of Pieter de Jong.

For further details see http://www.chori.org/bacpac/home.htm

VECTOR: PARALPS
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Submitted (17-JUN-2003) Wellcome Trust Sanger Institute, Hinxton, Submitted (17-JUN-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, Carb. 15A, UK. E-mail enquirises:
Cambridgeshire, Car. uk Clone requests: clonerequest@sanger.ac.uk
On Jun 17, 2003 this sequence version replaced gi:30350055.
Sequence from the Mouse Genome Sequencing Consortium whole genome Shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.
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                                                                                                                                                                                                                                                 BX248984 191884 bp DNA linear ROD 17-JUN-2003
Mouse DNA sequence from clone RP23-278P12 on chromosome 1, complete
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                      76234 AGAATTACACAGAACTTGGAGATTTTTAAAC 76264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
       83 CGAACTCCACGGAAACGTCTGCTCCTCAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
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1. .191884
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Mus musculus
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             Birren, B. Nusbaun, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Cocke, P., Corum, B., DeArellano, K., Collymore, A., Cocke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Farco, S., Ferrelara, P., Firederald, M., Gage, D., Galagan, J., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamaft, A., Kartetas, A., Kells, C., Landers, T., Levine, R., Macdonald, P., Marcho, M., Marbitt, R., Maclean, C., Macdonald, P., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mabbitt, R., Maclean, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Petreson, R., Phunkhang, P., Pierre, N., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Travers, M., Vassiliev, H., Venkataraman, V., Schubs, K., Zimmer, A. and Zody, M. Direct, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (26-SEP-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON Sep 13, 2003 this sequence version replaced gi:32328999. All repeats were identified using Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://ftp.genome.washington.edu/RM/RepeatMasker.html
Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone="RP23-249L15"
clone_lib="RPCI-23 Female Mouse BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="PCR product sequence only"
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complement(5491..5788)
/rpt_family="Lx5"
6490..6679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
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/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rpt_family="(TA)n"
complement(2224, .2904)
rpt_family="Lx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: L26921
Center clone name: 249_L15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="clone boundary
clone_end:SP6
site:EcoRI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96. .1631
rpt_family="Lx2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pt_family="Lx2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rpt_family="MTA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   map="1"
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124982 TAGTTATCTGTCACTGAATAAGGAATTATACCAGATTTTAGCAGCATCATGCAGAAACAC 125041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.9%; Score 30.2; DB 10; ilarity 58.2%; Pred. No. 60; Conservative 0; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 TCAGTCGCTCTCCGAACTCCACGGAAACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt family="(TA)n"
11107. .11222
/rpt family="Lx9"
complement (12336. .13145)
/rpt family="Lx"
14137. .1425
                                                                                                                                                                                                                                                                                                             rpt family="AT rich"
complement(10279. .10540)
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                                                                                                                                                                     /rpt_family="AT_rich"
complement(6695..8850)
/rpt_family="MT2B"
complement(8861..9036)
/rpt_family="Li PM"
complement(9037..9219)
/rpt_family="Li PM"
                                                                                                                                                                                                         family="L1_MM"
ement(9027
                                                                                                                                                                                                                                     family="MT2B"
ement (000)
                                                    /rpt_family="URRIA"
complement(8163, .8222)
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                                                                                                                                                                                                                                                                   complement (9204. .9336)
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                                                                                                            /rpt_family="(TATAA)n"
8461. .8630
                                                                                                                                         /rpt_family="(TATAA)n"
8658. .8678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="Lx2"
16191. .16218
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17488. .17665
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                                                                                                                                                                                                                                                                                                                                                                                                                            family="AT_rich" 3. .11085

    18765
    family="AT_rich"

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25756. .26039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                family="A-rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "RSINEL"
                                                                                                                                                                                                                                                                                                                                                                                     rpt_family="(TG)n"
0820..10862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'rpt_family="L1_MM"
12199. .22303
/rpt_family="L1_MM"
7376. .7403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="LIVL2"
5632. 1610

    17665 - family="LIMA7"

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5578. .25618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     family="(CA)n"
                                                                                                                                                                                                                                                                                                                                                                      "LX5"
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/rpt_family="Lx9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'rpt_family="Lx" 1987. .22198
                                         complement (7976
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0986. .21988
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2409.
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4659.
                               /rpt_
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Direct Submission

Submitted (19-5BP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor plaza, Houston, TX 77030, USA

On Sep 19, 2002 this sequence version replaced gi:21747328. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequening reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both and sequence and whole genome shotgun sequence only contigs will be indicated in the feature table.

Center: Baylor College of Medicine
Center code: BC//
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NOTE: This is a 'working draft' sequence It currently consists of 5 contigs. The true order of the pieces arbitrary. Gaps between the condings are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Molecular and Human Genetics, Baylor College of Medicine, One Alor Plaza, Houston, TX 77030, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Rattus norvegicus"
                               Baylor Plaza, Houston, TX 77030,
3 (bases 1 to 193304)
Rat Genome Sequencing Consortium.
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/db_xref="taxon:10116"
/clone="CH230-457M16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .1334
/note="wgs_contig"
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                                                                                                                                                 L93304 bp DNA linear HTG 19-SEP-2002 attus norvegicus clone CH230-457M16, *** SEQUENCING IN PROGRESS AC118868
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Direct Submission
Submitted (21-APR-2002) Human Genome Sequencing Center, Department
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                       DRAFT; HTGS_ENRICHED.
     125042 TIAGTALCTCTACCAGICTTAAAITTC 125072
                                                                                                                                                                                                                                                                             AC118868.3 GI:23194649
HTG; HTGS_PHASE1; HTGS_DRAFT; F
Rattus norvegicus (Norway rat)
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                                                                                                              RESULT 14
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RESULT 15 AC099298

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To Toases I to 239140)

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Marzny, D. Marzie, Merzker, M. Lee., Abramzon, S., Addms, C., Alder, J.,
Anyalabechi, V., Aughersker, M. Jees, A. Main, A., Agguiano, D.,
Anyalabechi, V., Aughersker, D. Barber, M., Barnstead, M., Benahmed, F.,
Bidden, D., Bandaranake, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswalo, K., Blayt, C., Blankenburg, K., Blyth, P., Brown, M.,
Cardens, V., Carter, K., Cherc, G., Chen, R., Calderon, E.,
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Bayila, M.L., Daugner, C., Dang, Y., Dinh, H., Davya, K.,
Bagan, A., Basotto, M., Hamil, C., Manilla, K., Danda, B., Baves, K.,
Bernandez, S., Filmay, M., Hangen, C., Frans, C.A., Rallar, T., Faria, G.,
Harvay, Y., Havlak, P., Haves, A., Henderson, N., Hernandez, M.,
Harray, Y., Havlak, P., Haves, A., Henderson, N., Hernandez, M.,
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Hollins, B., Howells, S., Hadun, S., Hune, J., Indhason, B., Johnson, B., Usakes, J.,
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Raylor, R., Poindexter, M., Perez, M., Perez, B., Perez, B., Perez, M., Perez, M., Rein, M.,
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ALUMYZYB 239140 bp DNA linear HTG 13-MAY-2003
Rattus norvegicus clone CH230-40116, WORKING DRAFT SEQUENCE, 5
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3 (bases 1 to 239140)
                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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HTG; HTGS_PHASE1; HTGS_DRAFT; F
Rattus norvegicus (Norway rat)
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                                                                                                                                                                                                                                    SOURCE
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Nat Genome Sequencing Consortium.

Direct Submission

Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Modecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 13, 2003 this sequence version replaced gi:25085778

The sequence in this assembly is a combination of BAC based reads and whole genome shorgun sequencing reads assembled using Atlas and whole genome shorgun sequencing reads assembled using Atlas (http://www.hgsc.hom.uc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence colly contigs will be indicated in the feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.h NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the fainshed sequence as soon as it is available and the accession number will be preserved.
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64407: gap of unknown length
223476: contig of 159069 bp in length
223576: gap of unknown length
227284: contig of 3708 bp in length
227384: gap of unknown length
31763: contig of 4379 bp in length
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4 239140: contig of 7277 bp in length.
Location/Qualifiers
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Center code: BCM
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Search completed: October 11, 2004, 10:08:24 Job time : 1129.5 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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October 11, 2004, 08:24:41 ; Search time 189 Seconds (without alignments) 2966.995 Million cell updates/sec Run on:

US-10-009-317A-31 132 1 ggacctcgtctactagtccc......cggttgacaatatttccgca 132 Title: Perfect score: Sequence:

Scoring table:

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6747726 Total number of hits satisfying chosen parameters:

3373863 seqs, 2124099041 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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ALIGNMENTS

ds, transcription factor; transgenic plant; growth rate; senescence; seed germination rate; plant vigor; seedling vigor. Plant yield-related polynucleotide clone G2520. ADD30447 standard; cDNA; 1197 BP. 09-AUG-2001; 2001US-0310847P. 19-NOV-2001; 2001US-0336049P. 11-DEC-2001; 2001US-033692P. 14-JUN-2002; 2002US-00171468. 09-AUG-2002; 2002WO-US025805. (first entry) Arabidopsis thaliana. WO2003013227-A2. 15-JAN-2004 20-FEB-2003 ADD30447; RESULT 1 ADD30447

(MEND-) MENDEL BIOTECHNOLOGY INC.

ö Riechmann JL, Adam LJ, Dubell AT, Heard JE, Jiang C, Reuber TL, Creelman RA, Pineda O, Yu Ratcliffe O, Pilgrim ML, J Broun PE;

New plant transcription factor polynucleotides and polypeptides, useful in producing transgenic plants with commercially valuable properties, such as an alteration in a plant growth characteristic, e.g. growth rate or apomixis. WPI; 2003-248221/24. P-PSDB; ADD30448.

Disclosure; SEQ ID NO 476; 454pp; English.

The invention relates to a number of isolated Arabidopsis thaliana cDNA sequences and their encoded proteins which are especially transcription factor related cDNA's and proteins. The isolated or recombinant plant transcription factor polymucleotides and polypeptides are useful in

and proteins. The isolated or recombinant plant transcription factor polymucleotides and polypeptides are useful in producing transgenic plants with commercially valuable properties, i.e. modified or altered desirable traits as compared to a reference plant, e.g. salt stress resistance, osmotic stress resistance, tolerance to freezing, drought, low humidity tolerance, or radiation resistance. Sequence information related to the polymucleotides and polypeptides can also be used in bioinformatic search methods. The transgenic plant is useful for growing a progeny plant from a parent plant. This sequence represents one of the CDNAs of the invention

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            modified or altered desirable traits as compared to a reference plant, such as an alteration in a plant growth characteristic, e.g. growth rate, germination rate of seeds, vigor of plants and seedlings, or leaf and flower senescence. Sequence information related to the polynucleotides and polypeptides can also be used in bioinformatic search methods. The transgenic plant is useful for growing a progeny plant from a parent plant. This sequence represents one of the cDNAs of the invention.
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producing transgenic plants with commercially valuable properties,
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                                                                                                                                 Sequence 1197 BP; 352 A; 224 C; 302 G; 319 T; 0 U; 0 Other;
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19-NOV-2001, 2001US-0336049P.
11-DEC-2001, 2001US-0336692P.
14-UTM-2002, 2002US-00171468.
                                                                                                                                                             23.5%;
56.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster expressed polynucleotide SEQ ID NO 31991.
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                                                                                                                                                                  Sequence 1197 BP; 352 A; 224 C; 302 G; 319 T; 0 U; 0 Other;
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Pred. No. 0.37;
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2000US-00614150
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P-PSDB; ABB68400.
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11-JUL-2000;
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The invention relates to a number of isolated cDNA sequences and their encoded proteins which are especially transcription factor related cDNA's

Disclosure; SEQ ID NO 37; 311pp; English

New plant transcription factor polynucleotides and polypeptides, useful in producing transgenic plants with commercially valuable properties, i.e. modified desirable traits, e.g. salt stress resistance or tolerance

Riechmann JL, Creelman RA, Keddie J, Pilgrim ML; Jiang C, Ratcliffe O, Pineda O, Yu G, Broun PB;

2003-248222/24.

Heard JE, Dubell AN,

WPI; 2003-248222/ P-PSDB; ADE31471.

(MEND-) MENDEL BIOTECHNOLOGY INC.

ó 1524 GGCCCGCGAAAAGTTGGCCCTGTACGTGTACGAATATCTGCTGCACGTTGGCGCCCAGAA 1583 . 1:8 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention issetul in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB116176-AB130511), expressed DNA sequences (AB116175) and the encoded proteins (ABB5737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell Gaps Drosophila melanogaster expressed polynucleotide SEQ ID NO 31988. developmental biology; cell signalling; insecticide; Sequence 6398 BP; 1456 A; 1470 C; 1528 G; 1944 T; 0 U; 0 Other; ó 22.4%; Score 29.6; DB 4; Length 6398; 61.8%; Pred. No. 2.5; ive 0; Mismatches 29; Indels 0. DB 4; Length 2817; Sequence 2817 BP; 885 A; 722 C; 746 G; 464 T; 0 U; 0 Other; Claim 1; SEQ ID NO 31988; 21pp + Sequence Listing; English. 29; Indels 1 GGACCTCGTCTACTAGTCCCTTACCGAGTAAGGAAATGTGCCGGACT from WIPO at ftp.wipo.int/pub/published_pct_sequences .Match
22.4%; Score 29.6; DB
Local Similarity 61.8%; Pred. No. 1.8;
les 47; Conservative 0; Mismatches EX, Myers BP. 1584 GGCGCACAGACATIC 1599 ABL12502 standard; cDNA; 6398 PWD, 23-MAR-2000; 2000US-0191637P. 11-JUL-2000; 2000US-00614150. 16 23-MAR-2001; 2001WO-US009231 (first entry) GGCGAAAGTCTCAGTC 걸 pharmaceutical; gene; ss Drosophila melanogaster. Venter JC, Adams M, WPI; 2001-656860/75. P-PSDB; ABB68399. (PEKE) PE CORP NY WO200171042-A2. 26-MAR-2002 Drosophila; 27-SEP-2001. 61 ABL12502; Query Match Query Match RESULT 4
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79038 chcdargacarcarcaaacradcadadarccdadccddagircrdacdaacdcarrcd 78979 ö 64 CTCGTCTACTAGTCCCTTACCGAGTAAGGAAATGTGCCGGACTTTTGCGGCGAGAAGGCG 0, DB 6; Length 82993; Indels 22.1%; Score 29.2; DB 6; 57.8%; Pred. No. 10; iive 0; Mismatches 38; AACGGCCCCGTGGCTCAACGAACAAGACGG 78949 65 AAAGTCTCAGTCGCTCTCCGAACTCCACGG 94 Query Match
Best Local Similarity 57.8'
Matches 52, Conservative 78978 g ò ò

RESULT 6 AA199682_21/c ContinuaTion (22 of 45) of AA199682 from base 2100001 (Mycobacterium tuberculosis strain

2234 GGCGCACAGACATIC 2219 16 61 GGCGAAAGTCTCAGTC g

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RESULT 5 ABX09140/c tD ABX09140 standard, DNA, 82993 BP.

(first entry) 08-APR-2003 Mycobacterium tuberculosis H37Rv BAC clone BAC-Rv221

val; virulence; protective antigen; vaccine; tuberculosis; leprosy; ds; cosmid. Mycobacterioses; survival; mycobacterial disease; tube

Mycobacterium tuberculosis

WO200274903-A2.

26-SEP-2002

22-FEB-2002; 2002WO-IB001973

22-FEB-2001; 2001US-0270123P.

(INSP) INST PASTEUR

Cole S;

WPI; 2002-759885/82

survival or virulence of mycobacteria the sequences of Mycobacterium Identifying and selecting genes for s by a comparative genomic analysis of tuberculosis and M. leprae.

Disclosure; Fig 4; 874pp; English

This invention relates to a novel method for identifying essential genes for survival or virulence of mycobacteria species. The method comprises aligning the genomic sequence of a first mycobacterium species on a genomic sequence of a second mycobacterium species on a polymucleotide sequence that is highly conserved in both genomes with no counterparts in other bacterial genomic sequences and that corresponds to an essential gene for the survival or virulence of mycobacterium species. The method of the invention is useful for detecting M. tuberculosis or N. leprae infection. The method reduces the number of potential new targets and protective antigens for new drugs and vaccine compositions to treat and prevent mycobacterial diseases, particularly tuberculosis and leprosy. The present sequence represents a Mycobacterial cosmid DNA sequence used in the method of the invention

Sequence 82993 BP; 14881 A; 26628 C; 26719 G; 14765 T; 0 U; 0 Other;

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1 GGACCTCGTCTACTAGTCCCTTACCGAGTAAGGAAATGTGCCGGACTTTTGCGGCGAGAA 2294 decececenana de indececentra de la companiera de la decece de la companie de

Best Local Similarity 61.8 Matches 47; Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 110000;
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Pred. No. 11;
0; Mismatches 38;
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  LOCUS AAI99682 Accession Aai99682
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                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77
                                                                                                                                                                                                                                                                                                                  mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.
                                                                                                                                                                                                                                                                              Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene. analvaing
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                                                                                                                                 Hayashi M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 21.8%; Score 28.8; DE Similarity 58.0%; Pred. No. 3.2; 51; Conservative 0; Mismatches
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                                                                                                                                 Mizoguchi H, Ando
Senoh A, Ikeda M,
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07-APR-2000; 2000JP-00159162.
03-AUG-2000; 2000JP-00280988.
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23-AUG-2000; 2000US-00649167.
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                                                                             (KYOW ) KYOWA HAKKO KOGYO KK
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Best Local Similarity
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                                                                                                                                 Nakagawa S,
Tateishi N,
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in game therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for generic disorders or other traits to assess biodiversity remains and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this parent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1699 GIGCCGTCCTTTCCTGCTTGGAGGCCAAGGCTGGGCTGGACTTCGAGCTCGACTCACT 1758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GIGCCGGACTITIGCGGCGAGAAGGCGAAAGTCTCAGTCGCTCTCCGAACTCCACGGAAA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brevibacterium lactofermentum; sucrose PTS enzyme II; sucrase; phosphoenolpyruvate:carbohydrate phosphotransferase system; glucose; coryneform bacterium; phosphoenolpyruvate-sugar transport system; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brevibacterium lactofermentum sucrose PTS enzyme II DNA SEQ ID NO:1.
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.8%; Score 28.8; DE 62.5%; Pred. No. 3.2; iive 0; Mismatches
                                                                                                                                            Claim 1; SEQ ID NO 17093; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
3779. .5764
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(first entry)
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Best Local Similarity 62.5'
Matches 45; Conservative
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20-APR-2001
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2001-639362/73. B; ABG17102. Φ

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85 AACTCCACGGAAACGTCTGCTCCTCAAA 112
Ozaki A;
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2410000
2510000
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Ikeda M,
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 Senoh A,
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                    WPI; 2001-376931/40.
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Continuation (13 of 45)
                                                                                                                                                                                                                                                                            Local Similarity
es 51, Conserv
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AA199682 00
AA199682 01
AA199682 03
AA199682 04
AA199682 05
AA199682 05
AA199682 06
AA199682 10
AA199682 10
AA199682 10
AA199682 10
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AA199682_28
AA199682_29
Tateishi N,
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Matches
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                                                                                                                                                                                                  PTS (phosphoenolpyruvate:carbohydrate phosphotransferase system or bhosphoenolpyruvate-sugar transport system) enzyme II, which has sucrose-binding activity. A coryneform bacteria produced with the sucrose PTS enzyme II gene can have more efficient sugar uptake, and improved amino-acid and nucleic acid productivity. The sucrose PTS gene and if's disrupted gene, such as one without the sucrose PTS function, can be used to produce new breeds of coryneform bacterial strains to uptake sugar more efficiently e.g. glucose only or and sucrose, and can have improved standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                     84
                                                                                                                 Gene encoding sucrose phosphoenolpyruvate-sugar transport system enzyme II obtained by cassette ligation-mediated amplification of downstream domain of coryneform bacterium sucrase gene, with sucrose-binding
                                                                                                                                                                                         present sequence encodes the Brevibacterium lactofermentum sucrose
                                                                                                                                                                                                                                                                                                                                                                                     CGAGTAAGGAAATGTGCCGGACTTTTGCGGCGAGAAGGCGAAAGTCTCAGTCGCTCTCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acid synthesis; vitamin; saccharide;
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                                                                                                                                                                                                                                                                                                                       Sequence 5969 BP; 1388 A; 1575 C; 1578 G; 1428 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                           DB 4; Length 5969;
                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C glutamicum coding sequence fragment SEQ ID NO: 7068.
                                                                                                                                                                                                                                                                                                                                                              37;
                                                               Kurahashi O;
                                                                                                                                                                                                                                                                                                                                                    Pred. No. 4.9;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                         21.8%; Score 28.8; ilarity 58.0%; Pred. No. 4.5 Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             85 AACTCCACGGAAACGTCTGCTCCAAA 112
                                                                                                                                                                      Claim 3; Page 22-29; 45pp; Japanese.
                                                              Sugimoto M, Nakamatsu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH68533 standard; DNA; 349980 BP
 30-JUN-2000; 2000WO-JP004348.
                    99JP-00189512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99JP-00377484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coryneform bacterium; amind organic acid synthesis; ds.
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                                         (AJIN ) AJINOMOTO CO INC
                                                                                  WPI; 2001-138150/14.
                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                            P-PSDB; AAB69080
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                    02-JUL-1999;
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                                                             Izui M,
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of AA199682 from base 1200001 (Mycobacterium tuberculosis strain;
15 fragments LOCUS AA199682 Accession Aai99682
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                                                                                                                                                                                                                                                                                                                                The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, meseuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium and abacteria are useful for producing amino acids, nucleic acids, vitamines, saccharides and organic acids, particularly 1-1ysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the Buropean Patent Office
Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 349980 BP; 81250 A; 97718 C; 90621 G; 80391 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGAGTAAGGAAATGTGCCGGACTTTTGCGGCGAGAAGGCGAAAGTCTCCGG
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                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 7068; 246pp + Sequence Listing; English.
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45607 GACTITCGCCAAGGCGCTGTCGGCGAIGCGCAAGCAGTTCGGCGGACACGCCGAGAAA 45666
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                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                    A TIGR (trabecular meshwork inducible glucocorticoid receptor) promoter.
                                                                                                                                                                                                                                                                                                                                                     TIGR; trabecular meshwork inducible glucocorticoid receptor; promoter; glaucoma; steroid sensitivity; progressive ocular hypertension; vision loss; ss.
                                                                                                                         2 GACCICGICIACIAGICCCTIACCGAGIAAGGAAAIGIGCCGGACTITIGCGGCGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diagnosis, prognosis and treatment of glaucoma, based on detecting specific polymorphisms in the promoter of the trabecular meshwork inducible glucocorticoid receptor gene.
                                                                      Score 28.4; DB 4; Length 110000;
Pred. No. 23;
0; Mismatches 46; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= c
/note= "GTGT added to produce TIGRmt3 mutant"
replace(5113, C)
/*tag= e
/note= "TIGRmt11 mutant"
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                                                                                                                                                                        62 GCGAAAGICICAGICGCICTCCGAACTCCACGGAAACGICTG 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= d
/note= "TIGRmt4 mutant"
replace(4337, G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/note= "TIGRmt1 mutant"
replace(4950, T)
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/note= "TIGRmt2 mutant"
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 4010000
4110000
4210000
4310000
4403765
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replace(4256, G)
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                                                                       21.5%;
ilarity 54.9%;
Conservative
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4100001
4200001
4300001
  3900001
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                                                                      Query Match
Best Local Similarity
Matches 56; Conser
AA199683_39
AA199683_40
AA199683_41
AA199683_42
AA199683_43
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07-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                   from base 1200001 (Mycobacterium tuberculosis strain
LOCUS AA199683 Accession Aai99683
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                                                                                                                                                                                                                                                  2 GACCTCGTCTACTAGTCCCTTACCGAGTAAGGAAATGTGCCGGACTTTTGCGGCGAGAAG 61
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                  Length 110000;
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                                                                                                                                                                                                Score 28.4; DB 4; Length 1
Pred. No. 23;
0; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                       46138 ccescraacraastosccreaceaastocaceaceacerces 46179
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fragments
Begin
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Best Local Similarity 54.9%;
Matches 56; Conservative
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3000001
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Continuation (13 of 44) of AA
WP Sequence split into 44 fra
WP AA199683 01
WP AA199683 01
WP AA199683 02
WP AA199683 04
WP AA199683 06
WP AA199683 10
WP AA199683 10
WP AA199683 11
WP AA199683 11
WP AA199683 12
WP AA199683 12
WP AA199683 15
WP AA199683 15
WP AA199683 15
WP AA199683 16
WP AA199683 22
WP AA199683 23
WP AA199683 24
WP AA199683 24
WP AA199683 24
WP AA199683 23
WP AA199683 33
 AA199682_30
AA199682_31
AA199682_33
AA199682_33
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AA199682_35
AA199682_39
AA199682_39
AA199682_39
AA199682_33
AA199682_33
AA199682_33
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glucocorticoid receptor) promoter, isolated from an individual without glucocorticoid receptor) promoter, isolated from an individual without prognosis and treatment of glaucoma, based on detecting specific polymorphisms in the promoter of the TIGR gene. The method is used for diagnosis and prognosis of glaucoma (of all types), steroid sensitivity and prognessive ocular hypertension that leads to loss of vision. Glaucoma can be treated by administering an agent that binds to ciscacting elements within the TIGR promoter. The TIGR promoter (or other regulatory regions) can be used to express homologous or heterologous genes, particularly for tissue-specific expression of therapeutic preming for tissue-specific monorate transcence animals and in screening for compounds (specific monorate transcence can be used as amplification primers or probes, e.g. for isolating related sequences in
meshwork inducible
   present sequence represents a TIGR (trabecular
                                                                                                                                                                                                                                                                                                                                                                                                                                 non-human animals
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Sequence 5271 BP; 1476 A; 1138 C; 1231 G; 1426 T; 0 U; 0 Other;

ö 2040 Tratreagractrararcreceagacaccagadadaaaardereagacaaagcagreacre 2099 80 21 TTACCGAGTAAGGAAATGTGCCGGACTTTTGCGGCGAGAAGGCGAAAGTCTCAGTCGCTC Gaps 0; Score 27.6; DB 3; Length 5 Pred. No. 13; 0; Mismatches 39; Indels Query Match 20.9%; Best Local Similarity 56.7%; Matches 51; Conservative d ò à

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AAV51361 standard; DNA; 5299 BP

AAV51361;

(first entry) 27-OCT-1998

Human TIGR promoter region DNA.

protein; human; diagnosis; glaucoma; polymorphism; steroid sensitivity; ss response trabecular meshwork induced glucocorticoid TIGR;

Homo sapiens

WO9832850-A1.

30-JUL-1998

98WO-US000468 09-JAN-1998;

97US-00938669. 28-JAN-1997; 26-SEP-1997;

(REGC) UNIV CALIFORNIA

Chen H; Chen P, Polansky JR, Nguyen TD,

WPI; 1998-427946/36.

protein (TIGR) promoter region which is used in a method for diagnosing glaucoma in a patient. The method involves the detection of polymorphisms whose presence is predictive of a mutation affecting TIGR response in the patient and can be diagnostic of glaucoma or steroid sensitivity. Base substitutions and base additions upstream of and within TIGR exons can Use of TIGR nucleic acid sequences - used for, e.g. developing products for diagnosis, prognosis and treatment of glaucoma. sequence is a trabecular meshwork induced glucocorticoid response Claim 34; Fig 1; 105pp; English. AAV51361
AAV

Sequence 5299 BP; 1482 A; 1151 C; 1235 G; 1431 T; 0 U; 0 Other; Length 5299; DB 2; Score 27.6; DE Pred. No. 13; 0; Mismatches also be used to diagnose glaucoma 20.9%; 56.7%; Conservative Local Similarity 51; Query Match Matches Best 8 X G

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Search completed: October 11, 2004, 09:30:40 Job time: 191 secs

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ALIGNMENT

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| Sequence 3.1 Application US/09309487 | Sequence 3.1 Application US/09309487 | Sequence 3.1 Application US/09309487 | Patent No. 6335318 | GENERAL INFORMATION: | APPLICANT: Selted, Michael E. | APPLICANT: Tang, Yi-Quan | APPLICANT: Yuan, Jun | APPLICANT: PURITION: Antimicrobial Theta Defensins and Methods of Using Same | FILE REFERENCE: P-UC 3095 | CURRENT FILING DATE: 1999-05-10 | NUMBER OF SEQ ID NOS: 31 | SEQ ID NO 31 | LENGTH: 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GECGAAAGTCTCAGTCGCTCTCCGAACTCCACGAAACGTCTGCTCCTCAAACGTTGAC 120
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US-09-967-808-31
Sequence 31, Application US/09967808
Sequence 31, Application US/09967808
Patent No. 6514727
GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Tang, Yi-Quan
APPLICANT: Yuan, Jun
APPLICANT: Ouellette, Andre J.
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
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APPLICANT: Selected, Michael E.
APPLICANT: Tang, Yi-Quan
APPLICANT: Yuan, Jun
APPLICANT: Vuent, Jun
APPLICANT: Vuent, Jun
APPLICANT: Outlette, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
FILE REFERENCE: P-UC 3095
CURRENT APPLICATION NUMBER: US/09/309,487
CURRENT FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
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TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using TITLE OF INVENTION: Same FILE REPERBNES: 9-UG 3095
CURRENT APPLICATION NUMBER: US/09/967,808
CURRENT FILING DATE: 2001-09-26
PRIOR PAPLICATION NUMBER: US/09/309,487
PRIOR FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3:
LENGTH: 132
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US-09-309-487-30
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Pred. No. 5.2e-31;
0; Mismatches 13; Indels 0;
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100.0%; Score 132; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.1e-39;
Matches 132; Conservative 0; Mismatches 0;
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Best Local Similarity 90.0%;
Matches 117; Conservative 0
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ORGANISM: Artificial Sequence
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US-09-309-487-30
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LENGTH: 132
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                                      Sequence 30, Application US/09967808
Patent No. 6514727
GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Tang, Yi-Quan
APPLICANT: Tang, Yi-Quan
APPLICANT: Vuan, Jun
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using
ITTLE OF INVENTION: Same
FILE REFERENCE: 2-UC 3095
CURRENT FILING DATE: 2001-09-26
CURRENT FILING DATE: 1999-05-10
FRICH APPLICATION NUMBER: US/09/309,487
PRICH APPLICATION NUMBER: US/09/309,487
PRICH SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 30
LENGTH: 132
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) OTHER INFORMATION: "n" bases at various positions throughout the sequence
) OTHER INFORMATION: represent a, t, c or g
US-08-103-840A-2
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APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: PERSER, Claire M.
APPLICANT: PERSER CLOINGER FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REPERENCE: 2436-20007.00
CURRENT APPLICATION NUMBER: U$/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
IENGTH 4403765
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ORGANISM: Artificial Sequence
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US-09-103-840A-2/c
RESULT 4
US-09-967-808-30
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US-09-103-840A-2
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: VENERE, John C.
; APPLICANT: VENERE, John C.
; TITLE OF INVENTION: TUBERCULOSIS
; TITLE OF INVENTION: TUBERCULOSIS
; TITLE OF INVENTION: UNMBER: US/09/103,840A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PATENTIN VEY: 2.1
; SEQ ID NO 2
; LENGTH: 4403765
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                                                                                               5 CTCGTCTACTACTCCCTTACCGAGTAAGGAAATGTGCCGGACTTTTGCGGCGAGAAGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VONTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
ENGTH: 4411529
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  Length 4403765;
                                                38; Indels
  DB 3;
                                                                                                                                                                                                                             2194589 AACGGCCCCGTGGCTCAACGACAAGACGG 2194560
Query Match .22.1%; Score 29.2; DE Best Local Similarity 57.8%; Pred. No. 8.5; Matches 52; Conservative 0; Mismatches
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                                                                                                                                                                                              65 AAAGTCTCAGTCGCTCTCCGAACTCCACGG 94
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ORGANISM: Mycobacterium tuberculosis
TOTHER INFORMATION: H37Rv
US-03-103-6408-1
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Patent No. 629428
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, ROBERT D.
                                                                                                                                                                                                                                                                                                                     RESULT 6
US-09-103-840A-1/c
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RESULT 9
US-09-306-828-34
US-09-306-828-34
Square 34, Application US/09306828
Square No. 6475724
GENERAL INFORMATION:
APPLICANT: NGUYEN, Thai D.
APPLICANT: Chen, Bua
APPLICANT: Chen, Bua
APPLICANT: Chen, Bua
TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis And
TITLE OF INVENTION: Nucleic Acids, Wits, And Methods For The Diagnosis And
CURRENT APPLICATION NUMBER: US/09/306,828
CURRENT FILING DATE: 1999-05-07
BARLIER APPLICATION NUMBER: US 09/227,881
BARLIER FILING DATE: 1999-01-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Microsoft Word 97
SEQ ID NO 34
LENGTH: 5271
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US-09-103-840A-1

| Sequence 1, Application US/09103840A
| Patent No. 6224328
| GENERAL INFORMATION:
| APPLICANT: FLEISCHWAN, Robert D. APPLICANT: FLEISCHWAN, Robert D. APPLICANT: WINTER, Ownen R. APPLICANT: VENTER, John P. APPLICANT: VENTER, John P. TITLE OF INVENTION: TUBERCULOSIS | TITLE OF INVENTION: TUBERCULOSIS | TITLE OF INVENTION: TUBERCULOSIS | FILE REPRENCE: 24366-20007.00 | CURRENT APPLICATION NUMBER: US/09/103,840A | CURRENT FILING DATE: 1998-06-24 | NUMBER OF SEQ ID NOS: 2 | SOFTWARE: Patentin Ver. 2.1 | SEQ ID NO 1 | CURRENT 4411529 | CURRENT 4411529 | CURRENT APPLICANT NUMBER OF SEQ ID NO 1 | CURRENT APPLICANT NUMBER OF SEQ ID NO 1 | CURRENT APPLICANT NUMBER OF SEQ ID NO 1 | CURRENT APPLICANT NUMBER OF SEQ ID NO 1 | CURRENT APPLICANT NUMBER OF SEQ ID NO 1 | CURRENT NUMBER OF SEQ ID NO 1 | CURRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GACCTCGTCTACTAGTCCCTTACCGAGTAAGGAAATGTGCCGGACTTTTGCGGCGAGAAG
                                                                                            0; Gaps
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DB 3; Length 4403765;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1245667 CCGGCTAACTAAGTCGCCTGACGAAGTCCACCACGACGTCGG 1245708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                      62 GCGAAAGTCTCAGTCGCTCTCCGAACTCCACGGAAACGTCTG 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46;
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Query Match 21.5%; Score 28.4; DB Best Local Similarity 54.9%; Pred. No. 16; Matches 56; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 21.5%; Score 28.4; DB
Best Local Similarity 54.9%; Pred. No. 16;
Matches 56; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37RV US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
CRGANISM: Homo sapiens
US-09-306-828-34
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RESULT 12
US-08-938-669A-2
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                                                                                                                                 2040 TTATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTG 2099
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                                              Gaps
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Query Match 20.9%; Score 27.6; DB 4; Length 5271; Best Local Similarity 56.7%; Pred. No. 2.6; Matches 51; Conservative 0; Mismatches 39; Indels 0
                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: NGUYEN, Thai D.
APPLICANT: Polansky, Jon R.
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,
TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND
TITLE OF INVENTION: RELATED DISEASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 5300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches 39; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,669A
                                                                                                                                                                                                           2100 CCCTACCTTCGTGGAGGTGACAGTTTCTCA 2129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Howrey & Simon
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
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CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/791,154
FILING DATE: 28-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mendelson, Biliot
REGISTRATION NUMBER: P-42,878
REFERENCE/DOCKET NUMBER: 07425-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 383-6857
                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08938669A Patent No. 6171788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5300 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 20004-2402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51; Conservative
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Best Local Similarity
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US-08-938-669A-1
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RESULT 11

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Patent No. 6475724
GENERAL INFORMATION:
Patent No. 6475724
GENERAL INFORMATION:
BAPLICANT: Mayuen, Thai D.
APPLICANT: Chen, Pu
APPLICANT: Chen, Pu
APPLICANT: Chen, Pu
APPLICANT: Chen, Hua
ITILE OF INVENTION: NUMBER: US/09/306, 828
CURRENT FILING DATE: 1999-05-07
CURRENT FILING DATE: 1999-01-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE NOS: 180
SOFTWARE MICROSOFT Word 97
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APPLICANT: Nguyen, Thai D.
APPLICANT: Nguyen, Thai D.
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,
TITLE OF INVENTION: RELATED DISEASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howrey & Simon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SUSTWARE: FastSEQ for Windows Version 2.0
SURRENT APPLICATION DATE: APPLICATION NUMBER: US/08/938,669A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2100 CCCTACCTTCGTGGAGGTGACAGTTTCTCA 2129
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FILING DATE:
FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/791,154
FILING DATE: 28-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mendelson, Eliot
REGISTRATION NUMBER: 9-42,878
REFERENCE/DOCKET NUMBER: 07425-/
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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ZIP: 2004-2402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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TELEX:
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 56.7<sup>3</sup>
Matches 51, Conservative
                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 1

LENGTH: 5300

TYPE: DNA

ORGANISM: Homo sapiens

US-09-306-828-1
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RESULT 15

US-09-306-828-3

Sequence 3, Application US/09306828

Patent No. 6475724

GENERAL INFORMATION:

APPLICANT: MUDYPEN, Thai D.

APPLICANT: Chen, Hua

TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And

TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And

CURRENT APPLICATION NUMBER: US/09/306,828

CURRENT FILING DATE: 1999-05-07

EARLIER FILING DATE: 1999-01-11

NUMBER OF SEQ ID NOS: 38

SOFTWARE: Microsoft Word 97

SEQ ID NO 3

LENGTH: 6169
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Pred. No. 2.8;
0; Mismatches 39; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 6169;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39;
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTENC FOR Windows Version 2.0
SUPTWARENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,669A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/791,154
APPLICATION NUMBER: 08/791,154
FILING DATE: 28-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mendelson, Elliot
REGISTRATION NUMBER: P-42,878
REGISTRATION NUMBER: P-42,878
REGISTRATION NUMBER: P-42,878
REGISTRATION NUMBER: P-42,878
TELEPONE: 202 383-6610
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Pred. No. 2.8;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 TCCGAACTCCACGGAAACGTCTGCTCCTCA 110
                                                                                                                                                                                                                                                                                                                                                                                    TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6169 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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ilarity 56.7%;
Conservative C
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Best Local Similarity 56.7%;
Matches 51; Conservative
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; ORGANISM: Homo sapiens
US-09-306-828-3
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Best Local Similarity
Matches 51; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09306828
Sequence 2, Application US/09306828
Batent No. 6475724
APPLICANT: Polansky, Jon R.
APPLICANT: Chen, Pu
APPLICANT: Chen, Hu
APPLICANT: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And CURRENT FILING DATE: 1999-05-07
CURRENT APPLICATION NUMBER: US/09/306,881
EARLIER APPLICATION NUMBER: US 09/227,881
BARLIER FILING DATE: 1999-01-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Microsoft Word 97
SEQ ID NO 2
LENGTH: 5304
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                                                                                                                                                                                                                                                                   21 TIACCGAGIAAGGAAAIGIGCCGGACTITIGCGGCGAGAAGGCGAAAAGTCTCAGICGCTC 80
                                                                                                                                                                                                                               21 TTACCGAGTAAGGAAATGTGCCGGACTTTTGCGGCGAGAAGGCGAAAGTCTCAGTCGCTC
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                                                                                                                                                  Length 5304;
                                                                                                                                                                                         Indels
                                                                                                                                              Query Match 20.9%; Score 27.6; DB 3; I Best Local Similarity 56.7%; Pred. No. 2.6; Matches 51; Conservative 0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                    2100 cccraccirceredagereacacircica 2129
                                                                                                                                                                                                                                                                                                              81 TCCGAACTCCACGGAAACGTCTGCTCCTCA 110
        ; SEQUENCE CHARACTERISTICS:
; LENGTH: 5304 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
;
US-08-938-669A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 5304
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-2
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2100 CCCTACCTTCGTGGAGGTGACAGTTTCTCA 2129

Search completed: October 11, 2004, 10:56:45 Job time: 51.5 secs

us-10-009-317a-31.rnpb

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October 11, 2004, 10:08:26; Search time 214 Seconds (without alignments) 3127.023 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                  1 ggacctcgtctactagtccc.......cggttgacaatatttccgca 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published Applications NA:*

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
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14: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
15: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
16: /cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*
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19: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*
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19: /cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                     OM nucleic - nucleic search, using sw model
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length: 2000000000
                                                                                                                                                                                                                                                     US-10-009-317A-31
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Perfect score:
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Maximum DB seq
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 31, Appl Sequence 30, Appl Sequence 47, Appl Sequence 443, App Sequence 645, App Sequence 645, App Sequence 2175, App Sequence 2175, App Sequence 2004, App Sequence 2604, App Sequence 262, App Sequence 3528, Appli Description 5 US-10-313-994-31 5 US-10-313-994-30 3 US-10-225-066A-479 6 US-10-225-066A-479 6 US-10-374-780A-443 5 US-10-080-170-645 6 US-10-080-170-645 6 US-10-369-493-36378 US-09-738-626-204 9 US-09-738-626-204 9 US-09-738-626-1 5 US-10-369-495-33481 6 US-10-369-495-33481 SUMMARIES Length DB 1000.0 82.7 82.7 23.5 23.5 23.5 22.1 22.1 22.0 21.8 21.8 21.5 21.5 Query Match Result No.

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		Sequence 3 Sequence 15 Sequence 16 Sequence 18 Sequence 3 Sequence 3 Sequence 3 Sequence 3	
424-599-6 437-963-3 224-633-9 298-633-1 224-633-1 224-633-1 244-633-2 244-633-3 087-192-1 087-192-1	99-916-955-74-99 99-8910-107-264 09-873-367C-865 09-998-598-59 09-918-998-1323 10-057-4758-1055 10-154-8848-1055	05-998-598-127 05-998-598-1219 10-998-598-1219 10-146-502-1519 10-146-502-1519 07-925-300-385 10-264-049-40 10-037-270-529 10-117-722-529 ALIGNMENTS	
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US-10-313-994-31

US-10-313-994-31

Sequence 31, Application US/10313994

Publication No. US20303062718A1

GENERAL INFORMATION:

APPLICANT: Selsted, Michael E.

APPLICANT: Tang, Yi-Quan

APPLICANT: Tang, Yi-Quan

APPLICANT: Vian, Jun

APPLICANT: Vian, Jun

TITE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same

FILE REFERENCE: P-UC 3095

CURRENT APPLICATION NUMBER: US/10/313,994

CURRENT APPLICATION NUMBER: US/09/309,487

PRIOR FILING DATE: 1999-06-10

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn Ver. 2.0

SOFTWARE: PatentIn Ver. 2.0

LENGTH: 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCGAAAGTCTCAGTCGCTCTCCGAACTCCACGGAAACGTCTGCTCCTCAAACGGTTGAC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ), OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Construct
US-10-313-994-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 132; DB 15; Best Local Similarity 100.0%; Pred. No. 1.7e-40; Matches 132; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Query Match 23.5%;
Best Local Similarity 56.3%;
Matches 58; Conservative
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, NAME/KEY: CDS

, LOCATION: (133)...(1197)

US-10-225-067-37
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APPLICANT: REUBER, T. Lynne
APPLICANT: REUBER, T. Lynne
APPLICANT: PINEDA, OMAINA
APPLICANT: PINEDA, OMAINA
APPLICANT: NU Guo-Liang
APPLICANT: NV Guo-Liang
APPLICANT: YOURNION: Yierre B
APPLICANT: PROUN, Yierre B
FILE REFERENCE: MB10036-2 US
                                                                                                                                                                                                                                                                            APPLICANT: Tang, Viller B.
APPLICANT: Tang, Viller B.
APPLICANT: Tang, Viller B.
APPLICANT: Yuan, Jun
APPLICANT: Yuan, Jun
APPLICANT: Vuen, Jun
APPLICANT: Outlette, Andre J.
APPLICANT: Outlette.
APPLICANT: Outlette.
TILLE GF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
FILE REFERENCE: P-UC 3095
CURRENT APPLICATION WHMBER: US/10/313,994
CURRENT FILING DATE: 2002-12-05
PRIOR APPLICATION WHMBER: US/09/309,487
PRIOR FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
LENGTH: 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GGCGAAAGTCTCAGTCGCTCTCCGAACTCCACGGAAACGTCTGCTCCTCAAACGGTTGAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GGTGAAAGTCTCAGTCGCTTTCCGAACTCCACGTAAACGTGTGCTCCTAAGACGGCAAAC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GGACCTCGTCTACTAGTCCCTTACCGAGTAAGGAAATGTGCCGGACTTTTGCGGCGAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Construct
US-10-313-994-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.7%; Score 109.2; DB 15; Length 132; 90.0%; Pred. No. 1e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LICATION NUMBER: US/10/225,066A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 479, Application US/10225066A Publication No. US20030226173A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Mendel Biotechnology, Inc.
APPLICANT: RATCLIFEF, Oliver
APPLICANT: RIECHMANN, Jose Luis
APPLICANT: ADAM, Luc J
APPLICANT: DUBBEL, ARNOLd T
APPLICANT: HEARD, Jacqueline B
APPLICANT: FIREME, Jacqueline B
APPLICANT: FIREMEN, Marsha L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/225
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 09/837,444
PRIOR FILING DATE: 2001-04-18
                                                                                                                                                                             Sequence 30, Application US/10313994
Publication No. US20030162718A1
GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
121 AATATTTCCGCA 132
                                            121 AATATTTCCGCA 132
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Best Local Similarity 90.0
Matches 117; Conservative
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US-10-225-066A-479
                                                                                                                                RESULT 2
US-10-313-994-30
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PRICE APPLICATION NUMBER: 6()136,049
PRICE APPLICATION NUMBER: 6()110,041
PRESENT: AP
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JULIORATION OF THE REPRESENTATION:

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JULIURE OF INVENTION:

JULIURE OF ORDER

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                                                                                                Sequence 645, Application US/10080170
; Sequence 645, Application US/10080170
; Publication No. US20030129601A1
; GENERAL INPORMATION:
; APPLICANT: COLE, S.T.
; TITLE OF INVENTION: DENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR TITLE OF INVENTION: TREATMENT OF WYCOBACTERIOSES
; TITLE OF INVENTION: TREATMENT OF WYCOBACTERIOSES
; TITLE OF INVENTION: UNBER: US/10/080,170
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/270,123
PRIOR PILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: Patentin Ver: 2.1
; SEQ ID NO 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79038 chcdangacacdicagcaaachadcgadafnccdadccddaghrchdacdaacdcannod 78979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 22.1%; Score 29.2; DB 15; Best Local Similarity 57.8%; Pred. No. 3.9; Matches 52; Conservative 0; Mismatches 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78978 AACGGCCCCGTGGCTCAACGAACAAGACGG 78949
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, ORGANISM: Mycobacterium tuberculosis
US-10-080-170-645
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; ORGANISM: Mycobacterium tuberculosis
US-10-080-170-645
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TTACCGAGTAAGGAAATGTGCCGGACTTTTGCGGCGAGAAGGCGAAAGTCTCAGTCGCTC 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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US-10-374-780A

US-10-374-780A

PUBLICALIN NO. US204001997A1

GENERAL INFORMATION NO. US204001997A1

APPLICANT: Riechman, Jose Luis

APPLICANT: Riechman, Jose Luis

APPLICANT: Riechman, Jose Luis

APPLICANT: Ratcliffe, Oliver

APPLICANT: Reuber, T. Lynne

APPLICANT: Pinde, Omaira

APPLICANT: Van GOU-Liang

FRIOR APPLICATION NUMBER: 06/310, 847

PRIOR APPLICATION NUMBER: 06/310, 649

PRIOR PILING DATE: 2001-06-19

PRIOR PILING DATE: 2001-11-11, 668

PRIOR PILING DATE: 2002-06-19

PRIOR PILING DATE: 2002-06-19
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                                                                                                                                                                                                                                1047 TAAGCATTGCAATGAACCGTTTGGTCAGCAAGCGTTTGAGAAT 1089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 TCCGAACTCCACGGAAACGTCTGCTCCAAACGGTTGACAAT 123
                                                                                                                                                                              81 TCCGAACTCCACGGAAACGTCTGCTCCTCAAACGGTTGACAAT 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
CTHER INFORMATION: G2520
US-10-374-780A-443
                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
US-10-374-780A-443
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25 CGAGTAAGGAAATGTGCCGGACTTTTGCGGCGAAGGCGAAAGTCTCAGTCGCCTCTCCG 84
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Pred. No. 1.9;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAL, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TAEDSHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR FILLING DATE: 1999-12-16
PRIOR FILLING DATE: 1999-12-16
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            320 CCGAAACTTCCTCTCCCAATATCTTGA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: JP 99/317484
PRIOR FILING DATE: 1999-12.16
PRIOR PELING DATE: 1999-12.16
PRIOR PELING DATE: 2000-04-07
PRIOR PELING DATE: 2000-06-03
PRIOR PELING DATE: 2000-06-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 2904
LENGTH: 1983
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PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
                                                                                                                                                                                          Sequence 2904, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium glutamicum
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Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                           APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MAZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOCHIAI, KEIKO
APPLICANT: YATEISHI, NAKO
APPLICANT: SENOH, AKIHIKO
APPLICANT: SENOH, AKIHIKO
APPLICANT: SENOH, AKIHIKO
APPLICANT: KENOH, AKIHIKO
APPLICANT: KEN
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ilarity 58.0%;
Conservative
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ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 51; Conserv
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US-09-738-626-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
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| GENERAL INFORMATION:
| APPLICANT: Cao, Yongwei
| APPLICANT: Hinkle, Gregory J.
| APPLICANT: Slater, Steven C.
| APPLICANT: Slater, Steven C.
| APPLICANT: Goldman, Barry S.
| APPLICANT: Chen, Xianfeng
| TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
| TITLE OF INVENTION: US/10/369,493
| CURRENT APPLICATION NUMBER: US/10/369,039
| PRIOR PILING DATE: 2002-02-21
| NUMBER OF SEQ ID NOS: 47374
| SEQ ID NO 36378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1034 AGGAAGTGGGTAGGCCTCTTCCCAGTTGAAGTAGCAGGCCTCCACCGCTGTCCGGAAGCC 975
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US-10-062-674-2175/C

Sequence 2175, Application US/10062674

Publication No. US20040005559A1

GENERAL INFORMATION:

APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.

TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS

FILE REFERENCE: PA-0026-1 CIP

CURRENT APPLICATION NUMBER: US/10/062,674

CURRENT FILING DATE: 2002-01-30

PRIOR PILING DATE: 2002-07-24

NUMBER OF SEQ ID NOS: 2217

SOFFWARE PERL PROGRAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 22.0%; Score 29; DB 16; Length 5493; Best Local Similarity 61.0%; Pred. No. 2.1; Matches 47; Conservative 0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
OTHER INFORMATĪON: Incyte ID No. US20040005559A1 814967.4
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COATION: (1) ... (5493)

COTHER INFORMATION: a, t, c, g, or other
US-10-062-674-2175
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US-10-369-493-36378/c
; Sequence 36378, Application US/10369493
; Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 ACGGAAACGTCTGCTCC 107
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; ORGANISM: Aspergillus nidulans
US-10-369-493-36378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 2175
LENGTH: 5493
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Sequence 34295, Application US/10369493
; Sequence 34295, Application US/10369493
; Sequence 34295, Application No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongworth Hinkle, Gregory J.
; APPLICANT: Glodman, Barry S.
; APPLICANT: Glodman, Barry S.
; APPLICANT: Glodman, EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROFERIES
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROFERIES
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROFERIES
; TITLE OF INVENTION: UNMBER: US 60/360,039
; CURRENT APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; FEMALES.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TILLE REPERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR PILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 47374
LENGTH: 2301
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21.2%; Score 28; DB 16; Length 2574;
Best Local Similarity 52.6%; Pred. No. 4.2;
Matches 61; Conservative 0; Mismatches 55; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 21.5%; Score 28.4; DB 16; Best Local Similarity 60.3%; Pred. No. 2.9; Matches 47; Conservative 0; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA; CRGANISM: Sphingomonas aromaticivorans US-10-369-493-34295
                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
, ORGANISM: Desulfitobacterium hafniense
US-10-369-493-33481
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; Sequence 66646, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: LA ROSA Thomas J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2168 ACCGGGCCGGAATTAAAC 2185
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US-10-198-846-9562/C

Sequence 9562, Application US/10198846

Publication No. US2003009974A1

GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, TITLE OF INVENTION: TOR IDENTIFICATION, ASSESSMENT, PREVENTION, TITLE OF INVENTION: TOWN UNMER: US/10/198,846
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
SOFTWARE: FESEZE for Windows Version 4.0

SEQ ID NO 9562

LENGTH: 882
                                                                                                                                                                                                                                                                                                                                                        25 CGAGTAAGGAAATGTGCCGGACTTTTGCGGCGAGAAGGCGAAAGTCTCAGTCGCTCTCCG
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                                                                                                                                                                                                                                                 Query Match
21.8%; Score 28.8; DB 9;
Best Local Similarity 58.0%; Pred. No. 16;
Matches 51; Conservative 0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2811729 TGCAACGCGTTTACGCCTCGTGCTCAAA 2811702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85 AACTCCACGGAAACGTCTGCTCCAAA 112
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9.10-369-493-33481
9.8cquence 33481, Application US/10369493
Publication No. US20030233675A1
9.GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
PAPPLICANT: Hinkle, Gregory J.
                                                                                                                                            TYPE: DNA; ORGANISM: Corynebacterium glutamicum US-09-738-626-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111 AACGGTTGACAATATTTC 128
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           PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 1
LENGTH: 3309400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Goy Vucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NOS 6646
LENGTH: 221
TYPE: DNA
ORGANISM: Glycine max
PREATURE: OTHER INFORMATION: Clone ID: PAT_MRT3847_31195C.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 GCCGGACTTTTGCGGCGAGAGGCGAAAGTCTCAGTCGCTCTCCGAACTCCACGGAAACG 99
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21.1%; Score 27.8; DB 13; Length 221;
Best Local Similarity 57.5%; Pred. No. 2.5;
Matches 50; Conservative 0; Mismatches 37; Indels 0,
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Search completed: October 11, 2004, 12:14:35 Job time : 217 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	sw model	October 11, 2004, 08:56:11; Search time 1398.5 Seconds (without alignments) 2818.597 Million cell updates/sec	
e version 3	sw model	3:56:11 ; (w. 28:	
GenCore (c) 1993	, using s	2004, 08	,
Copyright	OM nucleic - nucleic search, using sw model	October 11,	
	OM nucleic	Run on:	

1 ggacctcgtctactagtccc......cggttgacaatattccgca 132 US-10-009-317A-31 132 Perfect score: Sequence: Title:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

27513289 seqs, 14931090276 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

ESI: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	-			0001E-TOV 5/00004E	AA757359 ah96d12.s	BX437353 BX437353	AA392125 LD12495.5
	;	П		Dr.0880.14	AA757359	951 13 BX437353	AA392125
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4 6 0 8 8	107 107 107 107 107 107 107 107 107 107	330 330 348 366	7982 3304 3881 9866	10867046	AA331836 WGE247576 WGE003 N82289 N81726 BG657165 AAV703408	23 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
00000 00000	46844	128 128 138 138 138 138 138 138 138 138 138 13	0 1 10 10 6	27 H O H H O	7 1 1 1 1 1 1 0 4 4 4 4 5 0	4 C 4 4 4 4 4
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ALIGNMENTS

Homo sapiens (human)
Homo sapiens
Homo sapiens
Homo sapiens
Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota, Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 193)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,
Soares,F., Brentani,R.R., Reis,L.F., Orgeneel,C.V.,
Simpson,A.J. BF088574 130900-014-bl1 HT0881 Homo sapiens cDNA, mRNA sequence. BF088574.1 GI:10894284 Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Shotgun sequencing of the human transcriptome with ORF expressed sequence tags Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663 RESULT 1
BF086574/c
LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
CEYWORDS
SOUNCE
ORGANISM JOURNAL MEDLINE PUBMED COMMENT REFERENCE AUTHORS TITLE

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22.7%; Score 30; DB 13; Length 951;
llarity 45.9%; Pred. No. 99;
Conservative 17; Mismatches 23; Indels
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Matches 34; Conserva
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BX437353/c
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SOURCE
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                    /organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="txxxn:9606"

/db_xref="Adult"

/clone_lib="HT0881"

/clone_lib="HT0881"

/clone_frogan: head neck; Vector: puc18; Site_l: Smal;

/note="Organ: head neck; Vector: puc18; Site_l: Smal;

Site_2: Smal; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector: Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."
                                                            This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RCl-HT0881-130 900-014-bl1k23=2000-09-13&t4=1)  
Seq primer: puc 18 forward: 28  
High quality sequence start: 28  
High quality sequence store: 192.
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1 (Dases 1 to 397)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gancer Institute, Cancer Genome Anatomy Project (CGAP), Uppublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: capabs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 478 Std Error: 0.00
Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 391.
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ah96d12.s1 Soares NFL T GBC S1 Homo sapiens cDNA clone
IMAGE:1326935 3' Similar to gb:X59357 60S RIBOSOMAL PROTEIN L22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCICGICITACIAGICCCITACCGAGIAAGGAAAIGIGCCGGACTITIGCGGCGAGAAGG
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/db xref="taxon:9606"
/db xref="taxon:9606"
/dlone="IMAGE:1326935"
/lab host="PH10B"
/clone_lib="Soares_NFL_T_GBC_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                             Location/Qualifiers
1. .193
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AA757359
AA757359.1 GI:2805222
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56.0%;
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/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NDHL19W, testis NHT, and B-cell NCL_CGAP_CCB1) were mixed, and ss circles were made in vitro. POllowing HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302007, 682632-687239, 726408-72811, and 729096-731399. Subtraction by Bento Soares and M. Patima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
| hol_type="mRNA" |
| wol_type="mRNA" |
| wol_type="mRNA" |
| clone="CSCQRPOG6024" |
| tissue_type="THYMUS" |
| clone="Ibe = Homo sapiens THYMUS" |
| note="Vector: pCVNSpORT" |
| with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BX437353 Homo sapiens THYMUS Homo sapiens cDNA clone CSOCAP006YO24 5-PRIME, mRNA sequence.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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cgi-bin/cluster.cgi?seq-CSOCAPOOGBH120Pl&cluster=3181.f. Contact
cgi-bin/cluster.cgi?seq-CSOCAPOOGBH120Pl&cluster=3181.f. Contact
feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOCAPOOGBH120Pl.
Location/Qualifiers
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BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr. Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3181.f For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 TIACCGAGTAAGGAAAIGIGCCGGACTITITGCGGCGAGAAGGCGAAAGICTCAGICGCTC
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length EDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
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BX437353.1 GI:30777557
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us-10-009-317a-31.rst

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AQ034104
AQ034104.1 GI:3293724
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LD12495.Sprime LD Drosophila melanogaster embryo BlueScript
Drosophila melanogaster cDNA clone LD12495 Sprime, mRNA sequence.
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Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
I (bases 1 to 315)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lawrence Berkeley National Lab
Come Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit P element sequence 1(3)neo48-3
Plate: 124 row: H column: 11
High quality sequence stop: 256.
Location/Qualifiers
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                                                                                                                                                                                                                               888 TGAACAACSGTTCA 875
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AA392125
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| 1. .484 |
| /organism="brosophila melanogaster" |
| /organism="brosophila melanogaster" |
| /organism="brosophila melanogaster | lethal line" |
| /olone lib="brosophila melanogaster | lethal line" |
| /olone lib="brosophila melanogaster strains each of which contains a single pransposable element insertion that is thought to cause either lethality or sterility. The resultant fragment each strain was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://fruitfly.berkeley.edu/p_disrupt/inverse_por.html."
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Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Enkaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bohydroidea; Drosophilae; Drosophila.

Ephydroidea; Drosophilae; Drosophila.

Spradling, A.C., Stern, D., Beaton, A., Rehm, E.J., Laverty, T.,

Mozdan, N., Misra, S. and Rubin, G.M.

The BDG9 gene disruption project: Single P element insertions

mutating 30% of Drosophila autosomal genes

Unpublished (1998)

Contact: Gerald Rubin

Berkeley Drosophila Berkeley

LisA Building, Berkeley

LisA Building, Berkeley, CA 94720-3200, USA

Fax: $106439947

Email: gerry@fruitfly.berkeley.edu

Sequence recovery method was inverse PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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Drosophila melanogaster
Bukaryota, Metaroa, Arthropoda; Hexapoda, Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea, Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence orientation is forward strand relative to 5' end of element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 22.4%; Score 29.6; DB 28; Length 484; Best Local Similarity 61.8%; Pred. No. 1e+02; Matches 47; Conservative 0; Mismatches 29; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence is also known as STS Dm4324
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Location/Qualifiers
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/clone="LD43627"

/calone="LD43627"

/dev_stage="0 to 24 hours mixed stage embryonic"

/dev_stage="XL1 Blue"

/clone lib="LD Drosophila melanogaster embryo pOT2"

/note="Organ: embryo; Vector: pOT2; Site_1: EcoR1; Site_2:
Xhot; Sized fractionated cDNAs were directly ligated into pOT2.
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LD37723.Sprime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD37723 Sprime, mRNA sequence.
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/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_nost="%XL1 Blue"
/clone lib="LD Drosophila melanogaster embryo pOT2"
/clone lib="LD Drosophila melanogaster embryo pOT2"
/note="Organ: embryo; Vector: pOT2; Site_1: EcoR1; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
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Drosophila melanogaster
Enkaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Enkaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Enkaryota; Encaperyota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilade; Drosophila.

1 (bases 1 to 609)
Harvey,D.; Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Bocp/HHM Drosophila EST Project
Unpublished (2001)
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One Cyclotron Rd, Berkeley, CA 94720, USA
Pax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic sequence AC006495; hit P element sequence 1(3)neo48
Plate: 377 row: B column: 11
High quality sequence stop: 500.
Location/Qualifiers
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                                                                                                                                                                                                                                                                  Length 578;
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Pred. No. 1.1e+02;
0; Mismatches 29; Indels
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/db xref="taxon:7227"
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/clone="LD37723"
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Best Local Similarity 61.8
Matches 47; Conservative
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AIS18256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="male and female"
dev stage="0 to 24 hours mixed stage embryonic"
/lab_host="XL1 Blues"
/clone_lib="LD Drosophila melanogaster embryo pOT2"
/note="Organ: embryo; Vector: pOT2; Site 1: EcoR1; Site 2:
Xhol; Sized fractionated cDNAs were directly ligated into
pOT2.
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                    Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
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BDGP/HHMI Drosophila EST Project
Unpublished (2001)
                                                                                                                                                                Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic sequence AC006495; hit P element sequence 1(3)neo48
Plate: 441 row: D column: 10
High quality sequence stop: 522.
Location/Qualifiers
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hit genomic sequence ACO06495
Plate: 436 row: C column: 3
High quality sequence stop: 446.
Location/Qualifiers
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropodà; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                            organism="Drosophila melanogaster"
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:7227"
/clone="LD44146"
                                                                                                                    Contact: Stapleton, M. BDGP
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(bases 1 to 555)
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                                                                                             Unpublished (2001)
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I (Dades I to ) 11/10. Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Rall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond. D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project. Sanger Center, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: Darrell@sanger.ac.uk and
nh@sanger.ac.uk
constructed at the Institute for Genomic Research (TIGR),
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TRED927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution the library construction is
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects.
Barrell, School University Press, 1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .244
| organism="Oncorhynchus mykiss" |
| mal_type="mkNa" |
| mal_type="mkNa" |
| db xref="teaxon:8022" |
| clone="lRT3H05 B D03" |
| tissue type="myoled" |
| the host="Myoled" |
| host="NocCWA 1RT" |
| note="vector: pG/N SporT6; Site 1: Not1; Site 2: Sal1; |
| hote="rector and kidney." |
| spleen, muscle, and kidney."
                                                                                                                              Contact: Rexroad CE
USDA, ARS, National Center for Cool and Cold Water Aquaculture
USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Leetown Road, Kearneysville, WV 25430, USA
Tel: 304 725 0351
Email: crexroad@ncccwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified b
cross match v0.990329.
Seq primer: AGCGGATAACATTTCACACAGGA.
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                  1 (bases 1 to 244)
Rexroad,C.E. and Keele,J.W.
Sequence analysis of a rainbow trout normalized cDNA library
Unpublished (2002)
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T. brucei sheared genomic DNA clone 41c05, reverse sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trypanosoma brucei
Bukaryota, Buglenozoa, Kinetoplastida, Trypanosomatidae,
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llarity 62.2%; Pred. No. 1e+02;
Conservative 0; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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Email: nelsayed@tigr.org
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CA361075
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Oncorhynchus mykiss
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilade; Drosophila.

Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Endis,S. and Rubin,G.M.

Endopy,Brosophila EST Project
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit P element sequence 1(3) neo48-3[001],
Plate: 272 row: B column: 10
High quality sequence stop: 627.

1. 750
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/sex="male and female"
/dev stagge="0 to 24 hours mixed stage embryonic"
/lab_host="X11 Blue"
/clone_lib="LD Drosophila melanogaster embryo pOT2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (fruit fly)
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                                                                                            268 GGCGCACAGACATIC 283
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                                           GGCGAAAGTCTCAGTC
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3 ACCTCGICTACTAGTCCCTTACCGAGTAAGGAAATGTGCGGACTTTTGCGGCGAGAAAGG 62
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N60849.1 GI:1207000
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Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
_bocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                   AAAGTCTCAGTCGCTCTCCGAACTCCACGGAAACGTCTGCTCCTCAAACGGTTGACAATA 124
                                                                                                                                                                                                                                                                                                                                                                                 456 AAAGGATGGCTTCAACGCTGGAGATTGTGGGAAATATTGATTACCGCATCGTAGACAATA 515
                                                                                                                                                                                                                                                                             64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

1 (bases 1 to 1135)
Kremiczki,C., Higginbotham,J., Wylie,K., Carter,J., McPherson,J., Gallus gallus BAC End Reads
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_line="UCD001, inbred 256"
/clone_lib="CH261"
/note="Vector: pTARBAC2.1; Site_1: BcoR1; Site_2: EcoR1;
CH261 Female Chicken library - For library and clone
ordering information: http://www.chori.org/bacpac"
                                                                                                                                                                                                                                                                           CTCGTCTACTAGTACCCTTACCGAGTAAGGAAATGTGCCGGACTTTTGCGGCGAGAAGGCG
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                                                                                                                                                                                                    22.1%; Score 29.2; DB 29; Length 517; 52.5%; Pred. No. 1.4e+02; ive 0; Mismatches 58; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 182000 Std Error: 0.00
                                                                     /organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="41005"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Gallus gallus"
|mol type="genomic DNA"
|strain="Red Jungle Fowl"
|db xref="texcn:9031"
|clone="CH261-110A6"
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High quality sequence start: 127
High quality sequence stop: 556.
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                                                                                                                                                                                                                                         64; Conservative
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CC194385
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KEYWORDS
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/db xref="taxon:5811"
/clone="tgzy23h01.r1"
/lab host="x11-Blue MRF'"
/clone=lb="TgHT Tachyzoite CDNA"
/clone=lb="TgHT Tachyzoite CDNA"
/clone=lb="TgHT Tachyzoite CDNA"
/clone="Vector: Lambda ZAP; Site_1: ECORI; Site_2: XhoI;
/creskin fibroblast cultures in vitro. The library was
/constructed by KL. Wan, Cambridge University. CDNAs were
synthesized from polyA RNAs by oligo d(T) priming and
directionally cloned into the ECORI to XhoI sites of the
Lambda ZapII vector using the ZAP-CDNA synthesis kit
/stratagene). WARNING: the library contains a small
percentage of CDNAs derived from the human host cells."
                                                                                                                                                                                                                                                                                                                                                EST 22-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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744 ACCTCTTCAATACTTTCCTTACTAATTATGCGGCTGTGGCTCGCCTCTGCAACTC 803
                                                                                                                                                                                                                                                                                                                354 bp mRNA linear EST 22-MAY-200 TGSS7272723h01.rl TGRH Tachyzoite cDNA Toxoplasma gondii cDNA clone tgzy23h01.rl 5' similar to SW:Rl6C_ORYSA P46294 40S RIBOSOMAL PKOTEIN S16. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 GIGCAGACGIICGGCCGCAAGAAIGGAIGGGIIGCCGIICGCGCICIGNACIICAAGGCAAG 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: toxogwatson.wustl.edu
David Sibley at toxoest@borcim.wustl.edu for further information
relating to organism, clone or library availability.
Seq primer: T3
High quality sequence stop: 224.

Location/Qualifiers
| . 354 |
/ organism="Toxoplasma gondii" |
//mol_type="mRNA" |
/ strain="RNA" |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Toxoplasma gondii
Toxoplasma gondii
Ebkaryotan Alvoolata, Apicomplexa, Coccidia, Eimeriida,
Sarcocystidae, Toxoplasma.
1 (bases I to 354)
Hell, A., Manger, I., Marra, M., Sibley, L.D., Ajioka, J.A.,
Aslett, M.A., Dietrich, N., Dubuque, T., Hillier, L., Kucaba, T.,
Wan, K.L., Waterston, R.H. and Boothroyd, J.
Washd-Merck-Stanford-NIH Toxoplasma EST project
Unpublished (1996)
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WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.0%; Score 29; DB 14; Length 354;
.larity 62.9%; Pred. No. 1.40+02;
Conservative 0; Mismatches 26; Indels
                                                                             63 CGAAAGTCTCAGTCGCTCTCCGAACTCCACGGAAACGTCTGCTCCT
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completed: October 11, 2004, 10:55:09
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Nat. Genet. (2003) In press

Contact: Vidal Mac Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund May Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5139

Email: Marc Vidal@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project: Contact david_hill@dfci.harvard.edu or POLYÑ-No.
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                                      CB390295 412 bp mRNA linear EST 15-MAY-2003
OSTEL32B4_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="taxon:6239"
| db_xref="taxon:6239"
| fissue_type="whole animal"
| dev_stage="mixed stage"
| dev_stage="mixed stage"
| dov_stage="mixed stage"
| clone_lib="Ab-wrmcDDA"
| note="The AyrmcDDA library was generated with poly(A) + RNA isolated from both hermaphrodite and male N2 worms of subsequent generation of cDNAs of subsequent generation of cDNAs by poly(A) priming. The CDNAs were cloned into pPC86"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312 GATCÍTIGGAGCACGAÁTTCGAÁTGAATCAGTCATTCIGGGAGAGAGGTTCAAAACCTÍCIG 371
                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
[ (bases 1 to 412)
Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M.,
Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T.,
Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.
Endress,G.A., Janna,S., Chevet,E., Papasotiropoulos,V.,
Tolias,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
Doucette-Stamm,L., Hill,D.E. and Vidal,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 GACTITIGGGGGGGGAAAGGCGAAAGTCTCAGTCGCTCTCCGAAACTCCACGGAAACGTCTG
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HS 5004 Al F07 T7 RPCI11 Human Male BAC Library Homo sapiens
genomic clone Plate=580 Col=13 Row=K, genomic survey sequence.
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    412
    70xganism="Caenorhabditis elegans"
/mol type="mRNA"
/strain="N2"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQ332566
AQ332566.1 GI:4130193
GSS.
Homo sapiens (human)
                                                                                                                                                    Caenorhabditis elegans
Caenorhabditis elegans
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AQ332566/c
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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Email: jWallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Splate: S80 row: K column: 13
Seq primer: T7
Class: BAC ends
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria, Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 555)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Feller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell type="Lymphocytes"
/clone_lib="RPCI11 Human Male BAC Library"
/note="Vector: pBACe3.6; RPCI11 Human Male BAC Library"
                                                                                                                                                                      Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 GCGAAAGTCTCAGTCGCTCTCCGAACTCCACGGAAACGTCT 102
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/mol type="genomic DNA"
/db xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 555.
Location/Qualifiers
1..555
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Aah11967 Human sec
Aav84497 Human sec
Aba83280 Human sec
Ach04781 Novel hum
Acd44591 Human cDN
Ab189553 Human pol
Ach14641 Human cDN
Ad60107 Human pol
Ad67174 Nuclear f
Ad67174 Nuclear f
Ad7174 Nuclear f
Ad718635 Human imm
Aba16084 Human ner
Ab85635 Human imm
Aba16085 Human ner
Ab85636 Human ner
Ab87371 Human cDN
Ab103382 Drosophil
Ab11284 Brosophil
Ab112853 Drosophil
Ab112853 Drosophil
Ab112853 Drosophil
Ab1286340 Drosophil
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(without alignments)
2966.995 Million cell updates/sec
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                                                                                                                                                                                                                                              1 ggaccttgtctactagtccc......cggcaaacaatattacagtg 132
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5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                3373863 segs, 2124099041 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
  GenCore version (c) 1993 - 2004
                                                                                                                       October 11, 2004, 08:24:41;
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Maximum Match 100%
Listing first 45 summaries
                                                                                nucleic search, using sw model
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ABA83280
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ACH44781
ABL69553
AAH14641
AAC85535
AAC855535
AAC85555
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1: genesequi980s:*

3: genesequi990s:*

4: genesequi200s:*

5: genesequi2015s:*

6: genesequi2015s:*

7: genesequi2015s:*

8: genesequi203s:*

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length: 2000000000
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2852 33398 1373 1373 2889 2889 3482 3482	3276 E 4472 E 9391 E	Abg22915 Oligonucl Abg22914 Oligonucl Aaa75998 DNA encod Aa£87519 Human str Acc85077 Human MBC	9442 7871 1265
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AL I GNMENTS

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss. Yamamoto J; T; Saito K, Otsuki Ota T, Isogai T, Nishikawa T, Hayashi K, S. Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Human cDNA clone (3'-primer) SEQ ID NO:8802 ВÞ 29-JUL-1999; 99JP-00248036. 27-AUG-1999; 99JP-00300253. 11-JAN-2000; 2000JP-00118776. 09-JUN-2000; 2000JP-00183767. AAH11967/c ID AAH11967 standard; CDNA; 567 28-JUL-2000; 2000EP-00116126 (first entry) (HELI-) HELIX RES INST. WPI; 2001-318749/34. EP1074617-A2. Homo sapiens. 07-FEB-2001. 26-JUN-2001 AAH11967; RESULT 1

The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination

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Claim 3; SEQ ID NO 8802; 2537pp + Sequence Listing; English.

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complementary strand of a polymelectide which comprises a sequence and an oligonuclectide which comprises a sequence complementary to a polymuclectide which comprises a 3'-end sequence complementary to a oligonuclectide which comprises at 3'-end sequence complementary to a oligonuclectide comprises at least 15 nuclectides and the combination of the 5'-end sequence 15 selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polymuclectides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs and sequences; AAH03166 to AAH33628 and AAH33612 to AAH13613 to AAH13613 to AAH13613 to AAH13613 to AAH13613 represent human amino acid sequences; and AAH13629 to AAH13612 represent colligonuclectides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cerreacreceáceacerreceaacaacaaraacrecareceerrecerrereaarar 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 GAAAGTCTCAGTCGCTTTCCGAACTCCACGTAAACGTGTGCTCCTAAGACGGCAAACAAT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                370 cccaditercradgriricccaagaccacrirccreticgciriccaaaarggccrrrarc 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid molecules encoding 45 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 CCTTGTCTACTAGTCCCTTACCGAGTAAGGAAATGTACCGGACTTTTGCGGGGGAGAAGGT
oligonucleotide comprising a sequence complementary to the
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                                                                                                                                                                                                                                                                                                                                                                                        23.2%; Score 30.6; DB 4; Length 567; 52.8%; Pred. No. 0.37;
                                                                                                                                                                                                                                                                                                                                                   Sequence 567 BP; 172 A; 97 C; 177 G; 118 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                    59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC93348 standard; cDNA; 1679 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAR-1999; 99US-0126504P.
07-JAN-2000; 2000US-0174847P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    66; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTTC 306
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the fusion proteins AABS1380-B51431. The genes can be used to generate fusion proteins AABS1380-B51431. The genes can be used to generate fusion proteins by linking to the gene for the human common proteins by linking to the gene for the human control of the fusion protein as compared to the human protein only. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the disgnosis, treatment and prevention of: (a) cancer, e.g. breast and cancer, and other cancers of the addrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune discretes e.g. Addison's disease, allegyles, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) candiovascular discretial ischemias; (d) wound healing candiovascular discretial ischemias; (d) wound healing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 GAAAGTCTCAGTCGCTTTCCGAACTCCACGTAAACGTGTGCTCCTAAGACGGCAAACAAT 123
                                                                 The invention relate to the isolation of genes AAC93310-C93354 encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                  (£)
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                                                                                                                                                                                                                                                                                                                                                                                                                               (e) neurological diseases e.g. cerebral anoxia and epilepsy; and fectious diseases such as viral, bacterial, fungal and parasitic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.2%; Score 30.6; DB 3; Length 1679; 52.8%; Pred. No. 0.56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1679 BP; 383 A; 470 C; 388 G; 438 T; 0 U; 0 Other;
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                     Claim 1; Page 349; 410pp; English.
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97US-0048876P.
97US-0048877P.
97US-0048878P.
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06-JUN-1997;
06-JUN-1997;
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The invention relates to nucleic acid sequences (AAVB4411 to AAVB4633)

cocding human secreted proteins (AAWB8534 to AAWB6756). The secreted

protein gene sequences are deposited with the ATCC under deposit numbers

ATCC 97979, 97974, 97975, 97976, 97976, 209007, 209008, 209009, 209010,

COG 97979, 97974, 97975, 97976, 97977, 209007, 209008, 209009, 209010,

COG 97979, 97974, 97975, 97976, 97976, 209007, 209008, 209009, 209010,

COG 97979, 97974, 97975, 97976, 97976, 209007, 209008, 209009, 209010,

COG 000011, 209080, 209081, 209083, 209084, 209086, 209010,

COG 000011, 209080, 209081, 209083, 209084, 209087, 209010,

COG 0000110, 209080, 209081, 209083, 209084, 209087,

COG 0000110, 209080, 209081, 209082, 209083, 209081,

COG 0000110, 209080, 209082, 209083, 209083, 209083,

COG 000082, Alzheiner's and cognitive disorders, inclammation, allergies,

COG 000082, Alzheiner's and cognitive disorders, chizophrenia,

COG 000082, Alzheiner's and cognitive disorders,

COG 000082, Alzheiner's and cognitive disorders,

COG 000082, Alzheiner's and cognitive disorders,

COG 000082, Alzheiner's and cognitive disorders,
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Olsen HS, Ebner R, Brewer LA, Moore PA, Shi Y, Florence C; Florence K, Lafleur DW, Ni J, Pan P, Wei Y, Fischer CL, Soppet DR; Li Y, Zeng Z, Kyaw H, Yu G, Peng P, Dillon PJ, Endress GA; Carter KC;
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dermatological; immunosuppressive; antiinflammatory; immunostimulant;
cytostatic; cardiant; vascular; anti-angiogenic; ophthalmological;
                                                                                                                                                             New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.
                                                                                                 WPI; 1999-059865/05.
P-PSDB; AAW88620, AAW88841, AAW88642, AAW88843, AAW88844, AAW88845.
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23.2%; Score 30.6; DB 2; Length 1985;
Best Local Similarity 52.8%; Pred. No. 0.6;
Matches 66; Conservative 0; Mismatches 59; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1985 BP; 467 A; 542 C; 466 G; 506 T; 0 U; 4 Other;
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                                                                                                                                                                                                                               Claim 4; Page 347-348; 772pp; English.
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KW Huma

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97US-0070923P
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05-SEP-1997;
05-SEP-1997;
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06-JUN-1997;
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06-JUN-1997;
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ъ, Hu

Rosen CA,

Ruben SM,

Ferrie AM,

Greene JM,

Young P,

neuroprotective; nootropic; anticonvulsant; antialzheimers; vulnerary;

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proteins (I) and polynucleotide (II) sequences. (I) and (II) have various activities based on the tissues and cells the genes are expressed in. Example of these activities include: immunomodulatory; anticlerotic; dermatological; immunosupressive; antiinflammatory; immunostimulant; antipartinsonian; antimulant; antiantiant; antiantial antial antial argument, antipartinsonian; antimulant; antiparkinsonian; antimulant; and vulnerary. (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) can be used in the prevention, diagnosis and treatment of immune disorders (e.g. multiple sclerosis, systemic lupus erythematosus and human immunodeficiency virus (HIV) infections), hyperproliferative disorders (e.g. cancers and Gauchers disease), cardiomyopathy and coronary arteriosclerosis), angiogenic disorders (e.g. corneal graft neovascularisation and diabetic retinopathy), neurological disorders (e.g. Huntington's chorea, allowing wound healing, regeares), infectious diseases and value for promoting wound healing, regeneration and/or chemotaxis. ABAB18185 to the angelogical and parkinson's diseases (in the exemplification of the bosons of the angelogical disorders used in the exemplification of the angelogical disorders used in the exemplification of the angelogical disorders used in the exemplification of the angelogical disorders and the action of the angelogical disorders and the angelogical disorders and the action of the exemplification of the angelogical disorders and the action of the action of the angelogical disorders and the action of the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding 207 human secreted polypeptides, useful for preventing, diagnosing and/or treating, e.g. cancers, Parkinson's disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ni J, Ebner R, Lafleur DW, Moore PA, Olsen HS, Rosen CA; Ruben SM, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y; Florence C, Hu J, Li Y, Kyaw H, Fischer CL, Ferrie AM Fan Feng P, Endress GA, Dillon PJ, Carter KC, Brewer LA, Yu G,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 968-969; 1533pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                          21-FEB-2001; 2001WO-US005614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-FEB-2000; 2000US-0184836P.
29-MAR-2000; 2000US-0193170P.
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52.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preventing, diagnosing an and diabetic retinopathy.
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Greene JM;
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                                                                                                        (first entry)
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06-JUN-1997;
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                                                                                   ACH04781;
                                                     ACH0478
                                                                antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder; multiple sclerosis; systemic lugus erythematosus; HIV infection; cancer; human immunodeficiency virus; hyperproliferative disorder; wound healing; Gaucher's disease; cardiovascular disease; Scimitar syndrome; chemotaxis; corneal graft neovascularisation; diabetic retinopathy; regeneration; neurological disorder; Huntington's chorea; Alzheimer's disease; parkinson's disease; infectious disease; ss.
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Pred. No. 0.6;
0; Mismatches 59; Indels 0;
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Human; ss; gene therapy; autoimmune disorder; multiple sclerosis; cancer; systemic lupus erythematosus; haematopoietic cell disorder; allergy; agammaglobulinaemia; ataxia telangiectasia; blood coagulation disorder; affbrinogenaemia; thrombocytopenia; graft-versus-host disease; arthritis; inflammatory condition; ischaemia-reperfusion injury; infectious disease; hyperproliferative disorder; purpura; viral infection; regeneration; bacterial infection; ulcer; Alzheimer's disease; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human secreted protein #87 cDNA.
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124 ATTAC 128
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1523 cchicacheceadeacchiacecaacadanaadecigarecechiadecricidaarai 1582
                                                         1583 cccadiferencaderineceaagaceaenrecereregeeerneeaaaregeennare 1642
                                         64 GAPAGICTCAGGTTTCCGAACTCCACGTAAACGTGTGCTCCTAAGACGGCAAACAAT 123
     CCTTGTCTACTACTACCGAGTAAGGAAATGTACCGGACTTTTGCGGCGAGAAGGT
                                                                                                                                                                                              Human cDNA from novel secreted protein gene 87.
                                                                                                                                          ACD44591 standard; cDNA; 1985
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Moore PA, Shi Y, Florence C;
Fan P. Wei Y, Fischer CL, Soppet DR;
Peng P, Dillon PJ, Endress GA;
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970S-0057642P.
970S-0057643P.
970S-0057648P.
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P-PSDB; ABO44644.
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05-SEP-1997;
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(first entry)

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Human; ss; gene; secreted protein; precerebellin-like protein; neurodegenerative disorder; behavioural disorder; Alzheimer's disease; Parkinson's disease; Runtington's disease; schizophrenia; mania; dementia; paranoia; psychosis; autism; immune disorder; infection; inflammation; allergy; liver disorder; heparoblastoma; jaundice; hepatitis; immunological disorder; AlDS; leukaemia; rheumatoid arthritis; sepsis; acne; psoriasis; cancer.
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970S-0048878P.
970S-0048881P.
970S-0048881P.
970S-0048881P.
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970S-004899P.
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The invention relates to an isolated HEMAEBO protein. The protein is useful for preparing a composition for diagnosing or treating autoimmune disorders e.g. multiple sclerosis and systemic lupus erythematogus; disorders e.g. multiple sclerosis and systemic lupus erythematogus; classis and attaxia telangiectasia; blood coagulation disorders e.g. afibrinogenaemia and treamboortopenia; allergy; graft-versus-host disease; inflammatory conditions e.g. ischaemia-repertiation injury and arthritis; hyperproliferative disorders e.g. cancer and purpura; infectious disease; c.g. viral infection and bacterial infection. The polynucleotide or protein can be used to regenerate damaged tissue e.g. ulcers and Alzheimer's disease. The present sequence represents a novel human secreted protein cDMA. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from uspro.

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Query Match 23.2%; Score 30.6; DB 8; Length 1985; Best Local Similarity 52.8%; Pred. No. 0.6; Matches 66; Conservative 0; Mismatches 59; Indels 0;

Sequence 1985 BP; 467 A; 542 C; 466 G; 506 T; 0 U; 4 Other;

segdata.uspto.gov/sequence.html?DocID=20030065160

New isolated protein, useful for preparing a composition for diagnosing or treating cancer, inflammatory, immune or infectious diseases.

Example 1; SEQ ID NO 97; 172pp; English

rheumatoid arthritis, sepsis, acne, psoriasis) and cancer. The present sequence is one of the 238 disclosed cDMAs encoding a novel secreted protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at:- seqdata.uspto.gov/sequence.html?DocID=6525174B1

888888

Sequence 1985 BP; 467 A; 542 C; 466 G; 506 T; 0 U; 4 Other;

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Ruben SM, Rosen CA, Hu J;
Moore PA, Shi Y, Florence C;
Fan P, Wei Y, Fischer CL, Soppet DR;
Feng P, Dillon PJ, Endress GA;
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Olsen HS, Ebner R, Brewer LA,
Florence K, Lafleur DW, Ni J,
Li Y, Zeng Z, Kyaw H, Yu G, I
Carter KC;
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06-JUN-19997,
06-JUN-19997,
05-SEP-19997,
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05-SEP-1997;
05-SEP-1997;
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05-SEP-1997;
18-DEC-1997;
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05-SEP-1997
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The invention relates to an isolated protein comprising amino acid residues 33-205 or 1-205 of a a novel human secreted protein appearing as BAD26252. The protein is encoded by one of 238 disclosed cDNA sequences encoding 238 secreted proteins. ABD36252 is a precerbellin-like protein. Also included are a composition comprising the protein and a carrier and an isolated protein produced by expressing the protein cited above by a cell, and recovering the protein. The protein sare useful for diagnosing or treating neurodegenerative and behavioural disorders (e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, schizophrenia, mania, dementia, paranoia, psychoses or autism), immune disorders (e.g. hepatchlastoma, jaundice, hepatlitis), immunological disorders (e.g. AlDS, leukaemia, jaundice, hepatlitis), immunological disorders (e.g. AlDS, leukaemia,
New precerebellin-like protein, useful for diagnosing or treating neurodegenerative and behavioral disorders, immune disorders, liver
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The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the darenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital, (b) immune

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                                                                                                                                                                                                                                                                      64 GAAAGICICAGITICCGAACICCACGIAAACGIGIGCICCIAAGACGCAAACAAI
                                                                                                                                      4 CCTTGTCTACTACTCCTTACCGAGTAAGGAAATGTACCGGACTTTTGCGGCGAGAAGGT
                                                                       Gaps
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   Score 30.6; DB 8; Length 1985; Pred. No. 0.6;
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                                                                       59; Indels
                                                                       0; Mismatches
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23.2%;
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                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          124 ATTAC 128
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1587 1588 CCCAGTGTCTTCAGGTTTCCCAAGACCACTTCCCTGTGGGCTTCCAAAAATGGCCTTTATC 1647 disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infections diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length 64 GAAAGICICAGICGCITICCGAACTCCACGIAAACGIGICCTCAAGACGCAAAAAI 123 Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss. The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 1528 ccricaciccaccaccircaccaacagaraacicaarcacarcccriggcorreraarai 4 CCTIGICTACTAGICCCTTACCGAGIAAGGAAAIGIACCGGACITTIGCGGCGAGAAGGI 0; Gaps Yamamoto Match
Local Similarity 52.8%; Pred. No. 0.6;
es 66; Conservative 0; Mismatches 59; Indels 0; Claim 8; SEQ ID NO 12295; 2537pp + Sequence Listing; English. Sequence 1987 BP; 464 A; 548 C; 467 G; 507 T; 0 U; 1 Other; Isogai T, Nishikawa T, Hayashi K, Saito K, Sugiyama T, Wakamatsu A, Nagai K, Otsuki Human cDNA sequence SEQ ID NO:12295, AAH14641 standard; cDNA; 2510 29-JUL-1999; 99JP-00248036. 27-AUG-1999; 99JP-00300253. 11-JAN-2000; 2000JP-00118776. 02-MAX-2000; 2000JP-00183767. 09-JUN-2000; 2000JP-00241899. 28-JUL-2000; 2000EP-00116126 (first entry) (HELI-) HELIX RES INST WPI; 2001-318749/34. 1648 ATTTC 1652 124 ATTAC 128 EP1074617-A2. Homo sapiens, 26-JUN-2001 07-FEB-2001 Ś AAH14641; Query Match Ota T, Ishii S ω g g 8 ò à g

nucleotide sequences defined in the specification, where the cligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polyuncleotide which comprises a 5' end sequence and an oligonucleotide which comprises a 3' end sequence, where the comprises at least 15 nucleotides and the combination of the 5' end sequence/3' end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in cypenicalization. The primer sets can be used in antisense therapy and in cypericularly full-length cDNAs. The primers are also useful for the primers are useful for synthesising polynucleotides, comprised the primers and low obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC AAH13633 to AAH13632 represent human cDNA sequences; AAB92446 to AAB95893 crepresent human amino acid sequences, and AAH13632 represent colligonucleotides, all of which are used in the exemplification of the 2140 2141 ccchdigicittcadgifficcchdriccctdrogdctrcchapardgccrffarc 2200 GAAAGTCTCAGTCGCTTTCCGAACTCCACGTAAACGTGCTCCTAAGACGCCAAACAAT 123 2081 CCTTCACTCCCAGCACCTTGCCCAACAGGATAAGCTGGATCCCCTTGGCCTTCTGAATAT 4 CCTIGICIACIAGICCCTIACCGAGIAAGGAAAIGIACCGGACTITIGCGGCGAGAAGGI Human, nootropic, immunosuppressant; cytostatic; gene therapy; cancer peripheral nervous system; CNS; Alzheimer's, Parkinson's disease; Huntington's disease; harmington's disease; hameingtatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; . 0 / Match 23.2%; Score 30.6; DB 4; Length 2510; Local Similarity 52.8%; Pred. No. 0.66; nes 66; Conservative 0; Mismatches 59; Indels 0. Sequence 2510 BP; 574 A; 665 C; 630 G; 641 T; 0 U; 0 Other; Human polynucleotide SEQ ID NO 4096. RESULT 9 AA160107/c ID AA160107 standard; cDNA; 2793 BP. 99US-00471275. 2000US-00582117. 2000US-00582017. 2000US-0059042. 2000US-00650312. 2000US-00651450. 2000US-0065191. 2000US-0065191. 22-OCT-2001 (first entry) 2201 ATTTC 2205 124 ATTAC 128 present invention WO200153312-A1. 19-JUL-2000; 203-AUG-2000; 214-SEP-2000; 219-OCT-2000; 29-NOV-2000; 2 leukaemia; ss 26-DEC-2000; 21-JAN-2000; 25-APR-2000; 23-DEC-1999; 20-JUN-2000; Homo sapiens 26-JUL-2001 64 Query Match Best Loc Matches 82888888888888888888888888888888 셤 g a 8 8

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WO200157182-A2
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16-MAR-2000;
17-MAR-2000;
18-APR-2000;
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                                                                                                                                                  Matsuda A,
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                                                                                                                                                                                                                                                                                         The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM8642-AAM4213) with nootropic, immunosuppersant and cytostatic activity. The polymuclectides are useful in gene therapy. A composition containing a polypeptide or polymuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system classed neuropathies and central nervous system diseases, such as localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral solerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity, chemotextic/chemokinetic activity, haemostatic and thrombolytic activity, chemotextic/chemokinetic activity, haemostatic and thrombolytic activity, archer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
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                                          Wang D;
Zhao QA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
                                                                                                                                                                                        el nucleic acids and polypeptides, useful for treating disorders such central nervous system injuries.
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                                          Ren F,
Zhang J
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                                          Qian XB,
Yang Y,
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Xue AJ,
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Pred. No. 0.
                                      undi V, Chen R,
hrman T, Xu C, }
Drmanac RT;
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52.8%;
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                                        Liu C, Asundi V, Wang Z, Wehrman T
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Best Local Similarity 52.8
Matches 66; Conservative
                                                                                     Goodrich R,
                                                                                                                         WPI; 2001-442253/47
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(HYSE-) HYSEQ INC
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Zhou P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to novel proteins and their coding sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-KappaB). The proteins and their coding sequences are useful for treating a disease associated with NF-kappaB activation, such as inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases, or ischaemic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                             New purified protein that activates nuclear factor kappa B (NF-kappaB), useful for treating inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
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2000US-0184664P.
2000US-018350P.
2000US-0189874P.
2000US-0190076P.
03-DEC-2001; 2001JP-00368692.
05-DEC-2001; 2001JP-0038829P-
03-OCT-2002; 2002JP-00291302.
04-OCT-2002; 2002US-0415769P.
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2000US - 0205515P.
2000US - 021448PP.
2000US - 0216447P.
2000US - 0216447P.
2000US - 021748PP.
2000US - 021748PP.
2000US - 021748PP.
2000US - 0220964PP.
2000US - 0220969PP.
2000US - 02309PP.
2000US - 02309PP.
2000US - 023144PP.
2000US - 023149PP.
19-MAY-2000

20-JUN-2000

20-JU
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2000US-0241221P 2000US-024117885P 2000US-02411808P 2000US-02411808P 2000US-02418109P 2000US-02464714P 2000US-0246474P 2000US-0246474P 2000US-0246474B 2000US-024652B 2000US-024921B 2000US-024921B 2000US-024921B 2000US-024921B 2000US-024921B 2000US-024921B 2000US-024924B 2000US-025039B 2000US-025189B 2000US-025189B 2000US-02518B 20-0CT-2000; 20

GENOME HUMAN (HUMA-) Ruben Barash SC, Rosen CA,

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WPI; 2001-483426/52

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis

Listing; English Disclosure; SEQ ID NO 40447; 3071pp + Sequence AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleorides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For

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14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
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    21165 CCTTCACTCCCAGCACCTTGCCCAACAGGATAAGCTGGATCCCCTTGGCCTTCTGAATAT 21224
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example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) polymucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (1) proteins and polymucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK8764 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK4942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                 64 GAAAGTCTCAGTCGCTTTCCGAACTCCACGTAAACGTGTGCTCCTAAGACGGCAAACAAT 123
                                                                                                                                                                                                                                               4 CCTTGTCTACTACTCCTTACCGAGTAAGGAAATGTACCGGACTTTTGCGGCGAGAAGGT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; fimunosuppressive; antibiliflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; crebroprotective; antiinflammatory; antiallergic; antidiabetelic; antiluler; anticonvulsant; antidiapeteric; antilular, antiparastic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
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0
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Pred. No. 1.5;
0; Mismatches 59; Indels 0;
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02-MAR-2000; 2000US-0189550P.
17-MAR-2000; 2000US-0189674P.
17-MAY-2000; 2000US-0190076P.
18-APR-2000; 2000US-01913P.
19-MAY-2000; 2000US-0205515P.
07-UNY-2000; 2000US-0209467P.
28-UNN-2000; 2000US-0214886P.
30-UUN-2000; 2000US-021435P.
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04-FEB-2000; 2000US-0180628P
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                                                                                                                                                                                                            Local Similarity
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25-SEP-2000; 2000US-023497P; 25-SEP-2000; 2000US-0234997P; 26-SEP-2000; 2000US-023484P; 27-SEP-2000; 2000US-023584P; 29-SEP-2000; 2000US-023584P; 29-SEP-2000; 2000US-023586P; 2000US
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2000US-0225447P.
2000US-0225757P.
2000US-0225758P.
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22-AUG-2000) 2000US-0226868P.
22-AUG-2000) 2000US-0227182P.
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14-AUG-2000; 2000US-022513P.
14-AUG-2000; 2000US-022513P.
14-AUG-2000; 2000US-0225214P.
14-AUG-2000; 2000US-022526EP.
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01-SEP-2000; 2000US-0229344P.
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05-SEP-2000; 2000US-0229509P.
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08-SEP-2000; 2000US-0231242P.
08-SEP-2000; 2000US-0231243P.
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08-NOV-2000; 2000US-0246474P

08-NOV-2000; 2000US-0246475P

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17-NOV-2000; 2000US-0249214P

17-NOV-2000; 2000US-0249244P
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08-DEC-2000; 2000US-0251868F.

08-DEC-2000; 2000US-0251868F.

08-DEC-2000; 2000US-0251989F.

08-DEC-2000; 2000US-0251999F.

11-DEC-2000; 2000US-0251990F.
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2000US-0249297P.
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2000US-0250391P.
2000US-0251160P.
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2000US-0251988P.
2000US-0256719P.
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01-DEC-2000; 2
01-DEC-2000; 2
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Ruben SM Rosen CA, Barash SC,

WPI; 2001-541565/60

3224 human nervous system antigen polypeptides, diagnosing and/or treating nervous system cancers Nucleic acids encoding useful for preventing, and metastases.

Disclosure; SEQ ID NO 8415; 1701pp + Sequence Listing; English.

The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing

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21225 cccadidictrcaderricecadeaceacricecretedederrecaaardecerrare 21284
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; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                      64 GAAAGICTCAGGTTTCCGAACTCCACGTAAACGTGTGCTCCTAAGACGCAAACAAT 123
                                                                                                                                                               4 CCTTGTCTACTAGTCCCTTACCGAGTAAGGAAATGTACCGGACTTTTGCGGCGAGAAGGT 63
                                                                                                                                                                                           21165 ccirroacroccadoraccrisciccaacadearaagericearceccriscicerrordaarar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40448
                                                                                Sequence 22013 BP; 5294 A; 5048 C; 5035 G; 6636 T; 0 U; 0 Other;
                                                                                                                                    ..
                                                                                                             5; Length 22013;
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                                                                                                          Query Match 23.2%; Score 30.6; DB Best Local Similarity 52.8%; Pred. No. 1.5; Matches 66; Conservative 0; Mismatches
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2000US-0180528P.
2000US-0184664P.
2000US-0189774P.
2000US-0189774P.
2000US-0189774P.
2000US-01900765.
2000US-01900767.
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14-701-2000;
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14-AdG-2000;
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14-AUG-2000; 2000US-0225758P. 18-AUG-2000; 2000US-0225758P. 18-AUG-2000; 2000US-0226681P. 22-AUG-2000; 2000US-0226681P. 22-AUG-2000; 2000US-0226868P. 23-AUG-2000; 2000US-0227182P. 33-AUG-2000; 2000US-022709P. 30-AUG-2000; 2000US-022928PP. 01-SEP-2000; 2000US-022928PP. 01-SEP-2000; 2000US-0229344P.

01-SEP-2000; 2000US-0229345P 05-SEP-2000; 2000US-0229509P 05-SEP-2000; 2000US-0229513P

01-SEP-2000; 2 01-SEP-2000; 2 01-SEP-2000; 2

; 2000US-0230437P. ; 2000US-0230438P. ; 2000US-0231242P.

06-SEP-2000; 206-SEP-2000; 208-SEP-2000; 208

08-SEP-2000;

14-SEP-2000; 14-SEP-2000; 14-SEP-2000;

38-SEP-2000 -SEP-2000 SEP-2000 14-SEP-2000; 14-SEP-2000; 14-SEP-2000;

14-SEP-2000; 21-SEP-2000;

21-SEP-2000 25-SEP-2000

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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) and sequences given in AAM81170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polymucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polymucleotides may be used to produce the secreted (I). by inserting the nucleic acids into a host cell and culturing the cell to express the nucleic acids into a host cell and culturing the cell to express the diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic artisen genomic centers from the present invanted maximum elemantopoietic artisen genomic sequences from the present invantion. AAK54992 to AAK54950 and AAM82169 represent invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
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                                                                                                       17-NOV-2000; 2000US-0249211P
17-NOV-2000; 2000US-0249211P
17-NOV-2000; 2000US-0249212P
17-NOV-2000; 2000US-0249213P
17-NOV-2000; 2000US-0249214P
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             08-NOV-2000; 2000US-0246610P.
08-NOV-2000; 2000US-0246611P.
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17-NOV-2000; 2000US-0249207P.
17-NOV-2000; 2000US-0249208P.
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17-NOV-2000; 2000US-0249216P
17-NOV-2000; 2000US-0249217P
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17-NOV-2000;
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05-05C-2000;
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05-JAN-2001;
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27-SEP-2000; 27-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000;

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08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000;

2000US-0246524P.

38-NOV-2000;

2000US-0246532P

08-NOV-2000;

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21178 CCTTCACTCCCAGCACCTTGCCCAACAGGATAAGCTGGATCCCCTTGGACTTCTGAATAT 21237
                                                                                 21238 CCCAGTGTCTTCAGGTTTCCCAAGACCACTTCCCTGTGGGCTTTCCAAAATGGCCTTTATC 21297
                                                   GAAAGTCTCAGTCTCCGAACTCCACGTAAACGTGTGCTCCTAAGACGGCAAACAAT 123
                                                                                                                                                                                                                                                                                                                                                                               Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HTV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antishergic; antidiabetic; errebroprotective; antiinflammatory; antiparasitic; cardiant; immune disorder; cardiovascular disorder; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
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                                                                                                                                                                                                                                              ABA16085 standard; DNA; 22026 BP
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14-MUG-2000) 2000US-0218296.P.
14-MUG-2000) 2000US-02286.P.
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01-SEP-2000; 2000US-0229344P.
01-SEP-2000; 2000US-0229344P.
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06-SEP-2000; 2000US-0229344P.
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08-SEP-2000; 2000US-0231413P.
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Barash SC, Ruben SM;
17-NOV-2000; 2000US-0249211P.
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17-NOV-2000; 2000US-0249399P.
17-NOV-2000; 2000US-0249300P.
01-DEC-2000; 2000US-0251091P.
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05-DEC-2000; 2000US-025109P.
06-DEC-2000; 2000US-0256119P.
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08-DEC-2000; 2000US-0251868P
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05-JAN-2001; 2001US-0259678P
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Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases. invention relates to novel genes (ABA11004-ABA21534) and proteins Disclosure; SEQ ID NO 8416; 1701pp + Sequence Listing; English.

Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.

WPI; 2002-435328/46.

Claim 1; SEQ ID NO 142; 114pp; English.

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The interaction retailed for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and oversian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infections alseases such as wiral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form directly the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published_pot_sequences
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4 CCTTGTCTACTAGTCCCTTACCGAGTAAGGAAATGTACCGGACTTTTGCGGCGAGAAGGT 63

Matches

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viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriabais; rheumatoid arthritis; plomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                                   Human cDNA differentially expressed in granulocytic cells #142.
                                                                                                                                      granulocytic cell; DNA chip; bacterial infection;
                                                                                                                                                                                                                                                                                                                                  Vockley J;
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                                                                                                                                                                                                                                                                                                                                  Weissman SM, Yamaga
                                                              ABK83571 standard; cDNA; 175737 BP.
                                                                                                                                                                                                                                                                            03-OCT-2001; 2001WO-US030821.
                                                                                                                                                                                                                                                                                               03-OCT-2000; 2000US-0237189P.
                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                (GENE-) GENE LOGIC INC.
                 21298 ATTTC 21302
124 ATTAC 128
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                                                                                                                                                                                                                                        WO200228999-A2
                                                                                                  14-AUG-2002
                                                                                                                                                                                                                                                           11-APR-2002.
                                                                                 ABK83571;
                                                      ABK83571
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The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (GS) identified by DNA chip analysis as given in the specification, and comparing the expression level in an unactivated GC, where differential expression of GS is indicative of GCA. Also included are additioned in the capture of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in GS; (S) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation (especially chronic) or in a tissue, an allergic response in a classue, by contacting a tissue having inflammation (especially chronic) or in a tissue, an allergic response in a tissue, an allergic response in a tissue, an allergic response in a subject, to a pathogen or sterile inflammation (especially chronic) in a tissue, an allergic response in a subject to exposure of a subject to a pathogen or sterile inflammation (especially chronic) in a tissue, an allergic response in a subject, conscienting an especially chronic) in a tissue, an allergic response in a subject, conscients, and allergic response in a subject, conscients and a tissue, an allergic response in a subject, conscients and attended and arthritis, glomerulonephritis, asthma, thrombosis, checkpital or inflammatory distress syndrome, inflammatory bowel disease, Crohn's adult

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disease, ulcerative colitis, periodontal disease, also bacterial infection, viral infection, parabitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent not form part of the printed specification, but was obtained in electronic format directly from WIPO at fig.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                       Sequence 175737 BP; 41985 A; 43790 C; 42407 G; 47555 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 52.8%; Pred. No. 3.4;
Matches 66; Conservative 0; Mismatches 59; Indels 0;
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Sequence 1, Appli
                                                                          October 26, 2004, 15:20:02; Search time 31.5 Seconds (without alignments) 37.896 Million cell updates/sec
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Sequence 1,
Sequence 53
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-967-188-1
US-10-141-645-5
US-10-141-645-6
US-09-309-487-9
US-10-141-645-9
US-10-141-645-1
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US-10-141-645-4
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US-10-141-645-9
US-10-141-645-9
US-09-309-487-214
US-09-309-487-214
US-09-309-487-218
US-09-309-487-306
US-09-307-645-36
US-09-270-767-41896
                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                 478139 seqs, 66318000 residues
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Maximum Match 100%
Listing first 45 summaries
                                                     - protein search, using sw model
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1 GFCRCICTRGFCRCICTR 18
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Maximum DB seq length: 200000000
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Match Length DB
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No.
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APPLICANT: Selsted, Michael E. APPLICANT: Selsted, Michael E. APPLICANT: Selsted, Michael E. APPLICANT: Tang, Yi-Quan APPLICANT: Tung, Yi-Quan APPLICANT: Van, Jun APPLICANT: Ouelletto. Andre J. TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same FILE REPERBNCE: P-UC 3095
CURRENT APPLICATION NUMBER: US/09/309,487
CURRENT FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO I
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| Sequence 1, Application US/09967808 |
| Patent No. 6514727 |
| GENERAL INFORMATION: |
| APPLICANT: Selsted, Michael E. |
| APPLICANT: Yuan, Jun |
| APPLICANT: Yuan, Jun |
| APPLICANT: Yuan, Jun |
| TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using |
| TITLE OF INVENTION: Anmidicrobial Theta Defensins and Methods of Using |
| TITLE OF INVENTION: Anmidicrobial Theta Defensins and Methods of Using |
| TITLE OF INVENTION: Anmidicrobial Theta Defensins and Methods of Using |
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| TITLE OF INVENTION: Anmidicrobial Theta Defensions and Methods of Using 
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                 Sequence 37, Appl
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Sequence 7
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87.1%; Score 101; DB 3; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.3e-05;
Matches 15; Conservative 1; Mismatches 2; Indels
US-08-630-915A-37
US-09-879-957-37
US-09-252-991A-32502
US-09-252-991A-32301
US-09-608-438-30
US-07-906-349A-6
US-09-604-864-9
US-10-642-864-9
US-10-642-872-9
US-10-642-872-9
US-09-637-650B-5
US-09-637-650B-1
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US-09-309-487-1
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US-09-309-487-1
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; FEATURE:
; OTHER INFORMATION: synthetic variant
US-10-141-645-6
                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/09309487; Patent No. 6335318; GENERAL INFORMATION:
                                                                                                                                                                                                  1 GFCRCICTRGFCRCICTR 18
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                                                                                                           80.2%;
ORGANISM: Artificial Sequence
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                                                                                                  Query Match
Best Local Similarity 77.8%
Matches 14; Conservative
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COGANISM: Macaca mulatta
US-09-309-487-9
                                                                                                                                                                                                                                                                                                                RESULT 5
US-09-309-487-9
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                                                                                      Query Match 87.1%; Score 101; DB 4; Length 18; Best Local Similarity 83.3%; Pred. No. 1.3e-05; Matches 15; Conservative 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                   US-10-141-645-5

Sequence 5. Application US/10141645

Fatent No. 6713078

GENERAL INFORMATION:

APPLICANT: Robert Lehrer

APPLICANT: Alan Waring

APPLICANT: Alan Waring

APPLICANT: Alaxander Cole

APPLICANT: Teresa Hong

TITLE OF INVENTION: Retrocyclins - Antiviral and

TITLE OF INVENTION: Retrocyclins - Antiviral

TITLE OF INVENTION: Retrocyclins - Antiviral

CURRENT FLING DATE: 2002-06-06

PRIOR PILICATION NUMBER: 60/284,855

PRIOR FILING DATE: 2001-04-18

PRIOR FILING DATE: 2001-04-18

PRIOR FILING DATE: 2002-04-18

NUMBER OF SEQ ID NOS: 125

SEQ ID NO SEQ ID NOS: 125

LENGTH: 18

LENGTH: 18

LENGTH: 18

LENGTH: 18
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GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alexander Cole
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Altimicrobial Peptides
FILE REFERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: 60/284,855
PRIOR FILING DATE: 2002-05-06
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 18
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US-10-141-645-5
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ORGANISM: Artificial Sequence
; TYPE: PRT CRGANISM: Macaca mulatta US-09-967-808-1
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APPLICANT: Tang, Yi-Quan
APPLICANT: Tang, Xi-Quan
APPLICANT: Tang, Yi-Quan
APPLICANT: Van, Jun
APPLICANT: Outlette, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
FILE REFRENCE: P-UC 3095
CURRENT APPLICATION NUMBER: US/09/309,487
CURRENT PILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 18
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| Sequence 9, Application US/09967808
| Patent No. 514427|
| GENERAL INFORMATION:
| APPLICANT: Tang, Yi-Quan |
| APPLICANT: WINTENTION: Andre J. |
| TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using |
| TITLE OF INVENTION: Andre J. |
| TITLE OF INVENTION WINBER: US/09/967,808 |
| CURRENT FILING DATE: 1999-05-10 |
| PRIOR APPLICATION NUMBER: US/09/309,487 |
| PRIOR FILING DATE: 1999-05-10 |
| SOFTWARE: Patentin Ver. 2.0 |
| SEQ ID NO 9-10 |
| SEQ ID 
                                                                                                                                                        0; Gaps
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Best Local Similarity 81.2%; Pred. No. 0.00017;
Matches 13; Conservative 1; Mismatches 2; Indels
Score 93; DB 4; Lengtn 10,
Pred. No. 0.0001;
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Best Local Similarity 81.2%; Pred. No. 0.00017;
Matches 13; Conservative 1; Mismatches 2; Indels
                                                                                                                                                        1; Mismatches
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Ouery Match

75.0%; Score 87; DB 4; Length 18;
Best Local Similarity 72.2%; Pred. No. 0.00047;
Matches 13; Conservative 1; Mismatches 4; Indels
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US-10-14-645-2
; Sequence 2, Application US/10141645
; Sequence 2, Application US/10141645
; Patent No. 6133078
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Waring
; APPLICANT: Alan Waring
; TITLE OF INVENTION: Retrocyclins - Antiviral and
; TITLE OF INVENTION: Retrocyclins - Antiviral and
; TITLE OF INVENTION: Retrocyclins - Antiviral
; TITLE OF INVENTION: Retrocyclins - Antiviral
; TITLE OF INVENTION: Retrocyclins - Antiviral
; TITLE OF INVENTION: 2002-05-06
; FILE REFERENCE: UCLA-001CIP
; CURRENT APPLICATION NUMBER: Unassigned
; PRIOR PILING DATE: 2002-04-18
; PRIOR PILING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 125
; SEQ ID NO S: 125
; SEQ ID NO S: 125
; LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/10141645
Sequence 3, Application US/10141645
GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alexander Cole
APPLICANT: Alexander Cole
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT APPLICATION NUMBER: 06/284,855
PRIOR FILING DATE: 2002-06-06
PRIOR PILING DATE: 2000-04-18
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
; OTHER INFORMATION: synthetic variant
US-10-141-645-2
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                                                                                                                                                                             GENERAL INTEGRATION:
APPLICANT: Robert Lehrer
APPLICANT: Alexander Cole
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
TITLE OF INVENTION: Antimicrobial Peptides
TITLE OF INVENTION: Antimicrobial Peptides
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: Ussigned
PRIOR APPLICATION NUMBER: Unassigned
PRIOR PILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 53, Application US/09917340

Patent No. 669628

GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: Medaulty, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT PELLING DATE: 2001-07-29
PRIOR APPLICATION NUMBER: 60/221, 632
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-17-29
PRIOR FILING DATE: 2000-17-29
PRIOR FILING DATE: 2000-17-29
PRIOR FILING DATE: 2000-17-29
PRIOR FILING DATE: 2000-17-37
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 53
LENGTH: 18
                                                                                                                                Sequence 1, Application US/10141645
Patent No. 6713078
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; ORGANISM: Macaca mulatta
US-09-917-340-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 14; Conserv
                                                                                                            US-10-141-645-1
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LENGTH: 18
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Score 75; DB 4; Length 18;
Pred. No. 0.01;
0; Mismatches 6; Indels
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64.7%; Score 75; DB 4; Length 18;

Best Local Similarity 66.7%; Pred. No. 0.01;

Matches 12; Conservative 0; Mismatches 6; Indels
                    Sequence 8, Application US/10141645
; Sequence 8, Application US/10141645
; Patent No. 6713078
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Waring
; APPLICANT: Alan Waring
; APPLICANT: Alan Waring
; TITLE OF INVENTION: Retrocyclins - Antiviral and
; TITLE OF INVENTION: Attimicrobial Peptides
; TITLE OF INVENTION: Antimicrobial Peptides
; TITLE OF INVENTION: Antimicrobial Peptides
; TITLE OF INVENTION: Antimicrobial Peptides
; FILE REFERENCE: UCLA-001CIP
; CURRENT APPLICATION NUMBER: 60/284,855
; CURRENT FILING DATE: 2001-04-18
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO
; SEQ ID NO
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| Jacento No. 6713078
| Patent No. 6713078
| GENERAL INFORMATION:
| APPLICANT: Robert Lehrer
| APPLICANT: Alan Waring
| APPLICANT: Teresa Hong
| TITLE OF INVENTION: Antimicrobial Peptides
| FILE REPERENCE: UCLA-001CIP
| CURRENT APPLICATION NUMBER: US/10/141,645
| CURRENT PILING DATE: 2002-05-06
| PRIOR APPLICATION NUMBER: US/18
| PRIOR PILING DATE: 2001-04-18
| PRIOR FILING DATE: 2001-04-18
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 18
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COTHER INFORMATION: synthetic variant
US-10-141-645-9
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ORGANISM: Artificial Sequence
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Best Local Similarity 66.7%;
Matches 12; Conservative
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ORGANISM: Artificial Sequence
RESULT 13
US-10-141-645-8
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71.6%; Score 83; DB 4; Length 18;
Best Local Similarity 72.2%; Pred. No. 0.0013;
Matches 13; Conservative 0; Mismatches 5; Indels
              US-10-141-943-94

US-10-141-945-94

Patent No. 6713078

GENERAL INFORMATION:

APPLICANT: RObert Lehrer

APPLICANT: Alan Waring

APPLICANT: Alan Waring

APPLICANT: Alaxander Cole

APPLICANT: Teresa Hong

TITLE OF INVENTION: Retrocyclins - Antiviral and

TITLE OF INVENTION: Antimicrobial Peptides

TITLE OF INVENTION: Antimicrobial Peptides

TITLE PEREBENCE: UCLA-001CIP

CURRENT FILING DATE: 2002-05-06

PRIOR FILING DATE: 2001-04-18

PRIOR FILING DATE: 2001-04-18

PRIOR FILING DATE: 2002-04-18

NUMBER OF SEQ ID NOS: 125

SEQTUARE: FastSEQ for Windows Version 4.0

SEQTUARET: 18
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Sequence No. 6713078

GENERAL INFORMATION:

APPLICANT: Alan Waring

APPLICANT: Alan Waring

APPLICANT: Alexander Cole

APPLICANT: Alexander Cole

APPLICANT: Treesa Hong

TITLE OF INVENTION: Antimicrobial Peptides

TITLE OF INVENTION: Antimicrobial Peptides

FILE REFERENCE: UCLA-001CIP

CURRENT APPLICATION NUMBER: US/10/141,645

CURRENT FILING DATE: 2002-05-06

PRIOR PILING DATE: 2001-04-18

PRIOR APPLICATION NUMBER: Unassigned

PRIOR FILING DATE: 2002-04-18

NUMBER OF SEQ ID NOS: 125

SOFTWARE FEASER FASSED for Windows Version 4.0

SEQ ID NO 7
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; OTHER INFORMATION: synthetic variant US-10-141-645-7
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ORGANISM: Artificial Sequence
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1 GFCRCICTRGFCRCICTR 18

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Sequence 14, Application US/09967808 Patent No. 6514727
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Best Local Similarity 83.3%;
Matches 10; Conservative
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83.3%;
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
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Best Local Similarity 83.3
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                                                                                                                                                                                                                                 ; ORGANISM: Macaca mulatta
US-09-309-487-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
CORGANISM: Homo sapiens
US-09-309-487-29
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US-09-309-487-29
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US-09-967-808-14
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                                                                    RESULT 15
US-09-309-487-21
Sequence 21, Application US/09309487
Sequence 21, Application US/09309487
Sequence 21, Application US/09309487
GENERAL INPORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Tang, Yi-Quan
APPLICANT: Vaulette, Andre J.
TITLE OF INVENTYON: Antimicrobial Theta Defensins and Methods of Using Same
FILE REPRENCE: P-UC 3095
CURRENT APPLICATION NUMBER: US/09/309,487
CURRENT APPLICATION NUMBER: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
ENGURIP: 92
TENGRIP: 92
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Fatent No. 6514727

GENERAL INFORMATION:

APPLICANT: Seleted, Michael E.

APPLICANT: Tang, Yi-Quan

APPLICANT: Yean, Jun

APPLICANT: Yean, Jun

APPLICANT: Yean, Jun

APPLICANT: Yean, Jun

TITLE OF INVENTION: Same

FILE REFERENCE: PLC 3095

FILE REFERENCE: PLC 3095

CURRENT APPLICATION NUMBER: US/09/967,808

FILE RILNG DATE: 1999-05-10

FRIOR APPLICATION NUMBER: US/09/309,487

PRIOR FILING DATE: 1999-05-10

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 21

LENGTH: 92
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Pred. No. 0.062;
1; Mismatches 1; Indels
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Pred. No. 0.062;
1; Mismatches 1; Indels
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Patent No. 6335318
GENERAL INFORMATION:
APPLICANT: Seleted, Michael E.
1 GICICICGRGICYCICGR 18
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84.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 84.6%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 RCICTRGFCRCIC 16
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Best Local Similarity 84.6
Matches '11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 RCICTRGFCRCIC 16
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                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Macaca mulatta
US-09-309-487-21
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US-09-967-808-21
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US-09-967-808-21
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Sequence 29, Application US/09309487

Sequence 29, Application US/09309487

Sequence 29, Application US/09309487

Settle No. 6335318

Septent No. 6335318

Septent No. 6335318

Septent No. 6335318

APPLICANT: Selsted, Michael E.

APPLICANT: Youn, Jun

APPLICANT: Youn, Jun

APPLICANT: Will of NUMBER: June Jun

SETILE REFERENCE: P-UC 3095

CURRENT APPLICATION NUMBER: US/09/309,487

CURRENT FILING DATE: 1999-05-10

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 29

LENGTH: 76

LENGTH: 76
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APPLICANT: Tang, Yi-Quan
APPLICANT: Yuan, Jun
APPLICANT: Oublette, Jun
APPLICANT: Oublette, Jun
APPLICANT: Oublette, Jun
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
FILE REPREBLOR: P-UC 3095
CURRENT APPLICATION NUMBER: US/09/309,487
CURRENT FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 76
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GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Tang, Yi-Quan
APPLICANT: Tang, Yi-Quan
APPLICANT: Yuan, Jun
APPLICANT: Yuan, Jun
APPLICANT: Outlette, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using
TITLE OF INVENTION: AND 305
CURRENT APPLICATION NUMBER: US/09/967,808
CURRENT FILING DATE: 2001-09-26
PRIOR FILING DATE: 1999-05-10
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Pred. No. 0.54;
1; Mismatches 1; Indels
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Pred. No. 0.54;
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                                                                                              Gaps
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KUSIN, SARBARA K
MCWHERTER, CHARLES A
STATEN, NICHOLAS R
SUMMERS, NEENA L
BAUER, STEPHA C
LEE, STEPHO C
LIEP, STEPHO C
ASONISTS
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                                                 Score 64; DB 4; Length 76;
Pred. No. 0.54;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/510,238A
FILING DATE: 22-Feb-2000
CLASSIFICATION NUMBER: US/09/510,238A
FILING DATE: 22-Feb-2000
APPLICATION DATA:
APPLICATION NUMBER: W0 PCT/US 96/15774
FILING DATE: 06-OCT-1996
APPLICATION NUMBER: US 60/004,834
FILING DATE: 05-OCT-1995
ATTORNEY/AGBNT INFORMATION:
NAME: BENERT, DENNIS A
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: 2910/1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11arity 56.2%; Pred. No. 3; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: DENNIS A. BENNETT, G. CORPORATE PATENT DEPT
                                                                                                                                                                                                                                                                               Sequence 286, Application US/09510238A Patent No. 6730303 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 286:
SEQUENCE CHRACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: P.O. BOX 5110 CITY: CHICAGO STATE: ILLINOIS COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                         CAPARON, MAIRE H
ZURFLUH, LINDA L
                                                                                                                                                                                                                                                                                                                                              APPLICANT: FENG, YIQING BAUM, CHARLES M
                                                        Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
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CORRESPONDENCE ADDRESS
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Best Local Similarity
Matches 9; Conserva
; LOCATION: (1)...(20) US-10-141-645-15
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Sequence 29, Application US/09967808

Setent No. 6514727

GENERAL INFORMATION:
APPLICANT: Tang, Yi-Quan
APPLICANT: Yuan, Jun
APPLICANTION: Same
FILE REFERENCE: P-UC
AURENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US/09/309,487
PRIOR PLING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 29
LENGTH: 76
                                                                                                                                                  Gaps
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Pred. No. 0.54;
1; Mismatches 1; Indels
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SENERAL INFORMATION:
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
ITILE OF INVENTION: Retrocyclins - Antiviral and
ITILE OF INVENTION: Antimicrobial Peptides
ITILE OF INVENTION: Antimicrobial Peptides
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT FILING DATE: 2002-05-06
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: FastSEQ for Windows Version 4.0
SEGO ID NO 15
LENGTH: 76
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Pred. No. 0.54;
1; Mismatches
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83.3%;
                                                                                                           55.2%;
83.3%;
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Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                     Query Match
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                           4 RCICTRGFCRCI 15
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ORGANISM: Macaca mulatta
                              ; TYPE: PRT
; ORGANISM: Macaca mulatta
US-09-967-808-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
CRGANISM: Homo sapiens
US-09-967-808-29
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NAME/KEY: SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS-10-141-645-15
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US-09-967-808-29
            LENGTH: 76
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APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REPRENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: 60/284,855
FRIOR FILING DATE: 2001-04-18
FRIOR FILING DATE: 2002-05-06
FRIOR RELING DATE: 2002-06-18
FRIOR FILING DATE: 2002-06-18
FRIOR PRICE DATE: 2002-06-18
FRIOR PRICE DATE: 2002-06-18
FRIOR DATE: 2002-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                RESULT 23
US-003-309-487-18
US-003-309-487-18
Sequence 18, Application US/09309487
Sequence 18, Application US/09309487
GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Tang, Yi-Quan
APPLICANT: Tang, Yi-Quan
APPLICANT: Outellette, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
FILE REPREBRENCE: PUC 3095
CURRENT APPLICATION NUMBER: US/09/309,487
CURRENT FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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US-09-967-808-18

Sequence 18, Application US/09967808
Fatent No. 6514727
GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Tang, Y1-Quan
APPLICANT: Tang, Y1-Quan
APPLICANT: Yuan, Jun
APPLICANT: Yuan, Jun
APPLICANT: Yuan, Jun
APPLICANT: Andre J:
TITLE OF INVENTION: Same
FILE REPERENCE: P-UC 309;
FILE REPERENCE: P-UC 309;
GURRENT APPLICATION NUMBER: US/09/967,808
CURRENT FILING DATE: 2001-09-26
FRIDR APPLICATION NUMBER: US/09/309,487
FRIDR APPLICATION NUMBER: US/09/309,487
FRIDR APPLICATION NUMBER: US/09/309,487
SOFTWARE: PATENT OF 18
LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 50.0%; Score 58; DB 3; Length 9; Best Local Similarity 100.0%; Pred. No. 3.8e+05; Matches 9; Conservative 0; Mismatches 0; Indels
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US-10-141-645-36
'Sequence 36, Application US/10141645
'Patent No. 6713078
                    1 GFCRCICTRGFCRCIC 16
                                                                     8 GACCCACTTGCCTCTC 23
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; ORGANISM: Macaca mulatta
US-09-309-487-18
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PEATURE:
OTHER INFORMATION: generated by replacement of variants in consensus
OTHER INFORMATION: sequence
US-10-141-645-36
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48.3%; Score 56; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 3.88+05;
Matches 8; Conservative 1; Mismatches 0; Indels
                                                                                                                     Query Match 50.0%; Score 58; DB 4; Length 9; Best Local Similarity 100.0%; Pred. No. 3.8e+05; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Robert Lehrer
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral
TITLE OF INVENTION: Antimicrobial Peptides
FILE REPERBNCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT FILING DATE: 2002-05-06
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 49
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                         US-10-141-645-49; Sequence 49, Application US/10141645; Sequence 49, Application US/10141645; Setter No. 6713078; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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1 GFCRCICTRGFCRCICT
                                                         Query Match
Best Local Similarity 58.8
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 10; Conserv
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US-09-252-991A-32502
                   US-08-630-915A-37
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US-09-270-767-41896

Sequence 41896, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;

FILE REPRESENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-00-17

NUMBER OF SEQ ID NOS: 62517

SEQ ID NO 41896

LENGTH: 323

LENGTH: 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 37, Application US/08630915A

Patent No. 630920

GENERAL INPORMATICAN:
APPLICANT: SPARKS, Andrew B.
APPLICANT: FOWLKES, Dana M.
APPLICANT: KAY, Brian K.
APPLICANT: KAY, Brian K.
APPLICANT: KAY, Brian K.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
                                                                                                                                                                                                                                                                                                                                                                                                                Score 56, DB 4; Length 323;
Pred. No. 13;
1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-41896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEEE: Pennie & Edmonds LLP
?: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INPORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 FCRCICTRGFCRCICTR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 FCKSYCTFFFCRLFCAR 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 52.9%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1400 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: 11 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
STREET: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 28
US-08-630-915A-37
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APPLICANT: SPARKS, Andrew B.
HOFMAN, No. 6709821h
KAY, Brian K.
FOWLKES, Dana M.
MCCNNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
                                                 Gaps
                                                 1,
47.8%; Score 55.5; DB 3; Length 1400; 58.8%; Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.8%; Score 55.5; DB 4; Length 1400; 58.8%; Pred. No. 47; tive 0; Mismatches 6; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 11,174
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Jun-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-879-957-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                           Sequence 37, Application US/09879957
Patent No. 6709821
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1400 amino acids
                                                                                                                                        117 égcaccérgerc-cacr 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 GGCACCCTGGTC-CACT 132
                                                                                              1 GFCRCICTRGFCRCICT 17
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DB 1; Length 801;
                                                                                                                                                                                                                                                                                         47.4%; Score 55; DB 4; Length 2732;
57.1%; Pred. No. 90;
tive 0; Mismatches 6; Indels
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Best Local Similarity 55.6%; Pred. No. 39;
Matches 10; Conservative 0; Mismatches
          FILE REFERENCE: 0575/54806-A
CURRENT APPLICATION NUMBER: U3/09/086,436
CURRENT FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 30
LENGTH: 2732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-906-349A-6; Sequence 6, Application US/07906349A; Patent No. 5434064; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         345 GTCACCCTGTGACCCTCT 362
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INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 801 amino acids
                                                                                                                                                                                                                                                                                                                                                                                              3 CRCICTRGFCRCIC 16
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 5/...
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear y MOLECULE TYPE: protein US-07-906-349A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
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STRANDEDNESS: si
                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Murine
US-09-086-436-30
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| Patent No. 655195|
| Patent No. 655196|
| GENERAL INFORMATION:
| APPLICANT: Marc J. Rubenfield et al.
| APPLICANT: Marc J. Rubenfield et al.
| TILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PRIVENTION: NUMBER: US/09/252,991A
| TILE REFRENCE: 107196.136
| CURRENT PILING DATE: 1998-02-18
| PRIOR APPLICATION NUMBER: US 60/074,788
| PRIOR APPLICATION NUMBER: US 60/074,788
| PRIOR APPLICATION NUMBER: US 60/094,190
| PRIOR FILING DATE: 1998-07-27
| NUMBER OF SEQ ID NOS: 33142
| LENGTH: 565
| LENGTH: 565
| LENGTH: 565
Sequence 32502, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
APPLICANT:
MAC J. Rubenfield et al.
TITLE OF INVENTION:
APPLICANT:
APPLICANT:
OURRENT APPLICATION NUMBER:
US 60/074,788
PRIOR APPLICATION NUMBER:
US 60/074,788
PRIOR FILING DATE:
1998-02-18
PRIOR PLING DATE:
1998-02-18
PRIOR FILING DATE:
1998-07-27
NUMBER OF SEQ ID NOS:
33142
SEQ ID NO 32502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 30, Application US/09086436

Patent No. 6703486

GENERAL INFORMATION:
APPLICANT: Santoro, Bina
APPLICANT: Santoro, Bina
APPLICANT: Salegalbaum, Steven
APPLICANT: Tibbs, Gareth
APPLICANT: Tibbs, Gareth
APPLICANT: Tibbs, Tareth
APPLICANT: Tibbs, Tareth
TITLE OF INVENTION: Brain or Heart Cyclic Nucleotide Gated Ion Channel and
TITLE OF INVENTION: Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
47.4%; Score 55; DB 4; Length 168;
Best Local Similarity 61.5%; Pred. No. 10;
Matches 8; Conservative 2; Mismatches 3; Indels
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47.4%; Score 55; DB 4; Length 585;
Best Local Similarity 47.8%; Pred. No. 27;
Matches 11; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         532 GRCRALGTRGGKGWCVGCRCLCT 554
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                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150 CRCSRGPCRCACS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 CICTRGFCRCICT 17
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US-09-086-436-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           े
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APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: A NOVEL EXPRESSION-CLONING METHOD FOR
TITLE OF INVENTION: A REGET PROTEINS
TITLE OF INVENTION: IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE KINASES AND
TITLE OF INVENTION: ARGED PROTEINS
TORRESPONDENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: Z0004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATA:
MEDIUM TYPE: Floppy disk
COMPUTER: Date: 10 Porta: 10 Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/906,349A
FILING DATE: 30-JUN-1991
CLASSIFICATION DATA:
APPLICATION NUMBER: US/07/906,349A
FILING DATE: 18-JAN-1991
TELECOMMUNICATION INFORMATION:
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Sequence 8, Application US/09604864 Patent No. 6337317

GENERAL INFORMATION:

APPLICANT: Hancock, Robert E. W.
APPLICANT: Annock, Robert E. W.
APPLICANT: Annock, Lijuan
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES AND METHODS OF
TITLE OF INVENTION: USF THERSOF
FILE REFERENCE: UBC1170
CURRENT PELLING NUMBER: US/09/604,864
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 18

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DB 4; Length 1917;
                                                                                                                                                                                                                                                                                                                                                                46.1%; Score 53.5;
                                                                                                                                                                                                                                                                              ) ORGANISM: Caenorhabditis elegans US-09-627-650B-5
                                                                                                                                                                                                                                                                                                                                                                Query Match
Sequence 8, Application US/10042872
Patent No. 6747007
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hancock, Robert E. W.
APPLICANT: Zhang, Lilyann
TITLE OF INVENTION: USE THEREOF
TITLE OF INVENTION: USE THEREOF
CURRENT APPLICATION NUMBER: US/10/042,872
CURRENT FILING DATE: 2002-01-08
                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 09/604,864
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 19
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Gaps

.; 0

Length 18; 5; Indels

DB 3;

Score 54; DB Pred. No. 2.4; Mismatches

Query Match
Best Local Similarity 60.0%;
Matches 9; Conservative

; ORGANISM: Limulus polyphemus US-09-604-864-9

SEQ ID NO 9 LENGTH: 18

3 WCRYRCYRGFCRRFC 17

US-10-042-872-8

2 FCRCICTRGFCRCIC 16

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                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                   Score 54; DB 4; Length 18; Pred. No. 2.4; 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; DB 4; Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: THE UNIVERSITY OF BRITISH COLUMBIA

APPLICANT: HANGOCK, RODERT E. W.

APPLICANT: ADARGY, Lijuan

TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES AND METHODS OF

FILE REPERBACE: UBC1170-1

CURRENT APPLICATION NUMBER: US/10/042,872

CURRENT APPLICATION NUMBER: US/2000-01-08

PRIOR PILING DATE: 2000-01-08

PRIOR FILING DATE: 2000-06-27
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 8 LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-042-872-9; Sequence 9, Application US/10042872; Patent No. 6747007
                                                                                                                                                                                                                                                                       46.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.6%;
                                                                                                          ; TYPE: PRT
; ORGANISM: Limulus polyphemus
US-10-042-872-8
                                                                                                                                                                                                                                                                                                                                                                                                                    2 FCRCICTRGFCRCIC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 WCRRCYRGFCRYFC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
CRGANISM: Limulus polyphemus
US-10-042-872-9
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                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 60.03
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 38
US-09-627-650B-5
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Sequence 9, Application US/09604864
Patent No. 6337317
GENERAL INFORMATION:
APPLICANT: Hancock, Robert E. W.
APPLICANT: Zhang, Lijuan
TITLE OF INVENTION: UST THEREOF
FILE REFERENCE: UBC1170
CURRENT APPLICATION NUMBER: US/09/604,864
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 19
SOUTHWARE: FastSEQ for Windows Version 4.0

Gaps

. 0

Score 54; DB 3; Length 18; Pred. No. 2.4; 1; Mismatches 5; Indels

Query Match
Best Local Similarity 60.0%;
Matches 9; Conservative

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RESULT 35 US-09-604-864-9

; TYPE: PRT ; ORGANISM: Limulus polyphemus US-09-604-864-8

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Job time : 31.5 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bamber, Bruce
APPLICANT: Bamber, Bruce
APPLICANT: Bamber, Brik
APPLICANT: Borgensen, Erik
TILE OF INVENTION: Nematcode Neuromuscular Junction GABA Receptors and
TILE OF INVENTION: Methods Related Thereto
TILE OF INVENTION: Methods Related Thereto
TILE OF INVENTION: Methods Related Thereto
CURRENT APPLICATION NUMBER: US/09/436,063C
CURRENT FILING DATE: 1999-11-09
RIOR APPLICATION WUMBER: 60/107727
RIOR APPLICATION WUMBER: 60/107727
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5: 18
LENGTH: 1917
                                                      1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 46.1%; Score 53.5; DB 4; Length 1917; Best Local Similarity 60.0%; Pred. No. 1e+02; Matches 9; Conservative 0; Mismatches 5; Indels 1;
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60.0%; Pred. No. 1e+02; ative 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                 RESULT 39
US-09-436-063C-5
'Sequence 5, Application US/09436063C
'Patent No. 6407210
'GENERAL INFORMATION:
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, ORGANISM: Caenorhabditis elegans
US-09-436-063C-5
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ORGANISM: Caenorhabditis elegans
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                                                                                                                                              3 CRCICTRGFCRCICT 17
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    Best Local Similarity 60.09
Matches 9; Conservative
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US-09-627-650B-1
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

October 26, 2004, 15:15:31 ; Search time 23.5 Seconds (without alignments) 73.698 Million cell updates/sec Run on:

US-10-009-317A-32 Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 segs, 96216763 residues

Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% | Maximum Match 100% | Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	theta defensing	theta defensin la	ble integra		hypothetical prote	prot	inhibitor	trypsin inhibitor		ເກ			a.	hypothetical prote	7 - 7		ų,	proteinase inhibit	proteinase inhibit	proteinase inhibit	inhibi	hypothetical prote	ren-re	G protein-compled	restrictin predure	O300 protein - mon	hypothetical prote	in inhibitor	chondromodulin-I l
COLUMNIA	ΩI	1 0	A59089	E71602	G72858	T24272	T15651	JC1066	TIMB	S69207	807405	JC2225	TISYC2	S54581	T18975	A25964	S08167	TIZB1P '	TIZBIA	TIFB2	S07941	TISYD2	T25185	S32834	JC5042	JH0675	148725	PO0618	S56648	53
	DB	. 2	N	~	~	~		7										-	Н	-	~	-	~	~	0	н	0	N	a	7
	Length	18	16	4	σ	164	æ	73	72	419	83	94	0	624	152	157	1700	72	78	79	83	102	160	306	476	1353	77	550	113	317
de	당성	5.	'n.	•	ġ.	45.7	•	45.3	4.	4.	m.	•	43.5		٠	•	42.2	41.4	41.4		41.4	41.4	41.4	41.4	41.4	41.4	•		40.5	•
		87	64	54.5	54	53	Ŋ	52.5	51	ഗ	50.5	ö	ö	20	49	4.9	4	48	48	48	48	48	48	48	48	48	٠	47.5	47	47
	Result No.	1	7	m	4	Ω	φ	7	ω	σ	10	11	12	13	14	12	16	17	18	19	20	21	22	23	24	25	56	27	28	58

tenomodulin - mous hypothetical prote	hypothetical prote hypothetical prote on 330 protein prec	hypothetical prote related to mutanas	reelin precursor - proteinase inhibit - hypothetical prote	hypothetical prote hypothetical prote lafent transformin	unknown protein, 9 gene serrate prote	EF1 protein - fowl
JC7603 T34264	T15840 T22945 T42737	T33983 T49781	S58870 S09415 T17298	T09052 C96719 A57293	G96711 S16148	A31685
0 0	0,010	01 01 01	200	000	01 01	~
317	2946 3191 4660	141 883	3461 146 511	761 792 1251	1307	222
40.5	0.44 0.04 0.03 0.03	4.40 4.00 4.4.4	39.7 39.7	39.7 29.7	39.7	39.2
744	4 4 4 7 7 7	2.64.6	4 6 7 7 8 8 9	4 4 4 6 6 6	4 4 6 6	45.5
330	23 23 23 23 25 24	3 22	7 80 60 7 80 80 7 80 80	4 4 4 0 H G	4 4 4	45

ALIGNMENTS

RESULT 1 C59089 theta defensin-1 - rhesus macaque N;Alternate names: RTD-1 C;Species: Macaca mulatta (rhesus macaque) C;Becies: Macaca Mulatta (rhesus macaque) C;Accession: C59089 R;Tang, Y.Q.; Yuan, J.; Osapay, G.; Osapay, K.; Tran, D.; Miller, C.J.; Ouellette, A.J.; Schence 286, 498-522, 1999 A;Title: A cyclic antimicrobial peptide produced in primate leukocytes by the ligation of A;Reference number: A59089; MulD:99453140; PMID:10521339 A;Status: preliminary A;Molecule type: protein A;Residues: 1-18 (SEL> A;Molecule type: protein A;Residues: 1-18 (SEL> A;Note: acquence is cyclically permuted by -6 residues from the sequence presented is cyclically precursor sequences, see PIR:A59089 and PIR:B59089. C;Keywords: antibacterial; antibictic; antifungal; leukocyte; protein splicing C;Comment: For the two contributing precursor sequences. C;Keywords: antibacterial; antibictic; antifungal; leukocyte; protein splicing F;1-9/Region: theta defensin la-derived F;1-9/Region: theta defensin la-derived F;1-18/Cross-link: cyclopeptide (Arg-Cys) #status experimental F;2-11,4-9;13-18/Disulfide bonds: #status experimental F;2-11,4-9;13-18/Disulfide bonds: #status experimental	Query Match 75.0%; Score 87.0 DB 2; Length 18; Best Local Similarity 86.7%; Pred. No. 0.00014; Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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18

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1 RCICTRGFCRCLCRR 15 4 RCICTRGFCRCICTR

Theta defensin la precursor - rhesus macaque
C;Species: Macaca mulatra (rhesus macaque)
C;Species: Macaca mulatra (rhesus macaque)
C;Species: Macaca mulatra (rhesus macaque)
C;Accession: A59089
R;Tang, Y.O.; Yuan, J.; Osapay, G.; Osapay, K.; Tran, D.; Miller, C.J.; Ouellette, A.J.;
Science 286, 498-502, 1999
A;Title: A cyolic antimicrobial peptide produced in primate leukocytes by the ligation of
A;Reference number: A59089
A;Accession: A59089
A;Accession: A59089
A;Status: preliminary
A;Molecule type: mRNA
A;Rolecule type: mRNA
A;Rolecule type: mRNA
A;Residues: 1-76 c.TAN>
A;Cosa-references: UNIPROT:PB2270; GB.AF191100; NID:g6137227; PIDN:AAF04389.1; PID:g6137:C;Comment: For the complete mature sequence, see PIR:C59089.
C;Superfamily: mammalian defensin
C;Keywords: antibacterial; antibiotic; antifungal; leukocyte; protein splicing
F;1-20/Domain: signal sequence #status predicted <SIG>

Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative

à 음 RESULT 3

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hypothetical protein C27A2.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 10-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15651
R;Nhan, M.
Submitted to the EMBL Data Library, May 1996
A;Description: The sequence of C. elegans cosmid C27A2.
A;Reference number: 218382
A;Reference number: 218382
A;Reference number: 218382
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Retus: preliminary
A;Roses-references: UNIPPOT: Q18238; EMBL:U58760; NID:g1330384; PID:g1330389; PIDN:AAB0071
A;Experimental source: strain Bristol N2; clone C27A2
C;Genetics:
A;Gene: C5SP:C27A2.5
A;Map Position: 2
A;Introns: 19/3; 91/2
trypsin inhibitor - mung bean
C;Species: Vigna radiata (mung bean)
C;Accession: JC1066
R;Chen, C.Q.; Mao, J.F.; Zhang, M.F.; Dai, J.F.
C;Accession: JC1066
A;Accession: JC1066

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.7%; Score 53; DB 2;
50.0%; Pred. No. 6.9;
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Best Local Similarity 50.0
Matches 9; Conservative
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Best Local Similarity 50.0
Matches 9; Conservative
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A;Residues: 1-248 <GAR>
A;Cross-references: UNIPROT:096282; GB:AE001428; GB:AE001362; NID:93845316; PIDN:AAC7197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1.290 <AYR>
A;Cross-references: UNIPROT:P41470; GB:L22858; NID:g510708; PIDN:AAA66700.1; PID:g559139
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: E71602
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743; PMID:9804551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Note: dsDNA virus
C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
C;Dates: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
C;Accession: G2858
R;Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
Virology 202, 586-605, 1994
A;Title: The complete DNA sequence of Autographa callfornica nuclear polyhedrosis virus.
A;Reference number: A72850; MUID:94303173; PMID:8030224
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable integral membrane protein PFB0950w - malaria parasite (Plasmodium falciparum)
C.Species: Plasmodium falciparum
C.Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
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A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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                    F;21-64/Domain: amino-terminal propeptide #status predicted <PRO>F;74-76/Domain: carboxyl-terminal propeptide #status predicted <CTP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AcOrf-70 protein - Autographa californica nuclear polyhedrosis virus
C;Species: Autographa californica nuclear polyhedrosis virus, ACMNPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
46.6%; Score 54; DB 2; Length 290;
Best Local Similarity 40.7%; Pred. No. 7.7;
Matches 11; Conservative 2; Mismatches 4; Indels
                                                                                                                                    Score 64; DB 2; Length 76;
Pred. No. 0.2;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein T01B7.8 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 60.0%; Pred. No. 6;
Matches 9; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 FARCFCINTMOCFCPROGYKCECICRR 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 FCRCICT-----RGF-CRCICTR 18
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163 CSCICT---CTCICS 174

A, Gene: Acorf-70

RESULT 5 T24272

3 CRCICTRGFCRCICT 17

à

A; Experimental source: clone 3D7

A,Gene: PFB0950w

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A;Molecule type: protein
A;Residues: 'X',104-120 <JOU2>
R;Lee, J.; Gray, A.; Yuan, J.; Luch, S.M.; Avraham, H.; Wood, W.I.
submitted to the EMBL Data Library, December 1995
A;Description: Vascular endothelial growth factor related protein (VRP): A ligand and spé
A;Reference number: S69208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A)Cross-references: UNIPROT: P01063; EMBL: M20732; NID:g169944; PIDN: AAA33953.1; PID:g1699. A,Note: the sequences of codons 8-13 and 14-27 are interchanged in the authors' translat: R;Back, Mim, Sin. S.I. submitted to the EMBL Data Library, October 1992
A;Description: Nucleotide sequence of a cDNA encoding the soybean Bowman-Birk proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteinase inhibitor (Bowman-Birk) C-II - soybean
C;Species: Glycine max (soybean)
C;Species: Glycine max (soybean)
C;Date: 02-Dec-1993 #sequence revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: 8.29608; $529608; $740113
R;Joudrier, P.E.; Foard, D.E.; Floener, L.A.; Larkins, B.A.
Plant Mol. Biol. 10, 35-42, 1987
A;Title: Isolation and sequence of cDNA encoding the soybean protease inhibitors PI IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X76727; NID:g436413; PIDN:CAA54144.1; PID:g436414
C;Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
C;Keywords: serine proteinase inhibitor
F;22-48/Domain: Bowman-Birk inhibitor repeat homology <BBI>
F;49-74/Domain: Bowman-Birk inhibitor repeat homology <BBI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A)Gene: GDB:VEGFC; VRP
A)Cross-references: GDB:3890883; OMIM:601528
F;1-12/Domain: signal sequence #status predicted <SIG>
F;1-3.102/Domain: propeptide #status predicted <PRO>
F;13-102/Domain: propeptide #status predicted <PRO>
F;103-419/Product: vascular endothelial growth factor C #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X68705; NID:g18567; PIDN:CAA48656.1; PID:g18568
R;Giordano, A.; Delledonne, M.; Fogher, C.; Marchetti, S.
submitted to the EMBL Data Library, December 1993
A;Description: Nucleotide sequence encoding a soybean C-II proteinase inhibitor.
                                                                                                                                                                      A,Accession: S69208
A,Molecule type: mRNA
A,Residues: 1-419 -4208
A,Cross-references: EMBL:U43142; NID:g1150988; PIDN:AAA85214.1; PID:g1150989
R,Morris, J.C.
B,Accession: G02659
A,Reference number: H01557
A,Accession: G02659
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Residues: 1-419 -400R.
A,Residues: 1-419 -400R.
A,Cross-references: EMBL:U58111; NID:g1373426; PIDN:AAB02909.1; PID:g1373427
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 CRCICTR-----GFCRCICT 17
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A;Accession: S07405
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A;Accession: S40113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-83 <JOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-83 <BAE>
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A;Molecule type: DNA
A;Residues: 1-83 <GIO>
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d Lys-1, respectively
C;Comment: This inhibitor stoichiometrically inhibits trypsin in a molar ratio of 1:2.
C;Comment: This inhibitor stoichiometrically inhibits trypsin in a molar ratio of 1:2.
C;Comment: This inhibitor serine proteinase inhibitor.
E;13-39/Domain: Bowman-Birk inhibitor repeat homology <BB2>
F;40-65/Domain: Bowman-Birk inhibitor repeat homology <BB2>
F;40-65/Domain: Bowman-Birk inhibitor repeat homology <BB2>
F;20-65/Domain: Bowman-Birk inhibitor repeat homology <BB2>
F;20/Inhibitory site: Lys (trypsin) #status predicted
F;47/Inhibitory site: Arg (trypsin) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Note: three isoinhibitors are also found whose amino ends differ slightly from that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: mRNA A;Roseidues: 70-419 <70U1>
A;Note: this sequence has been revised in reference S69207
A;Accession: S74443
                                                                                        <u>ښ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2
                                                                                                                                                                                                                                                                                                                                    Crypsin inhibitor (Bowman-Birk) - mung bean (Species: Vigna radiata (mung bean) (Species: O'gna radiata (mung bean) (C)Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004 (C)Accesion: A01301 (R)Zhang, Y: Luo, S: Tan, F: Qi, Z: Xu, L: Zhang, A. Si. Sin. 25, 268-277, 1982 A; Title: Complete amino acid sequence of mung bean trypsin inhibitor. A;Reference number: A01301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vascular endothelial growth factor C precursor - human
NiAlternate names: FLT4 ligand DHM
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 27-Apr-1996 #sequence revision 01-Nov-1996 #text_change 09-Jul-2004
C;Accession: $69207; $61795; $71443; $69208; $60259
EMBO J. 15, 1751, 1996
A;Tille: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is A;Reference number: $69207; MUID:96203094; PMID:8612600
                                                                                        Gaps
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                                                                                     Indels
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                  Score 52.5; DB Pred. No. 4.6; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.0%; Score 51; DB 1
57.9%; Pred. No. 6.8;
iive 2; Mismatches
                                                                                                                                       3 CR-CICTR---GFCRCI----CTR 18
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                                                                                                                                                                   |: ||||| | |||;
CKSCICTRSMPGKCRCLDTDDFCTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Molecule type: protein
A,Residues: 1-72 <ZHA>
A,Cross-references: UNIPROT:P01062
                      45.3%;
            Query Match
Best Local Similarity 48.0°
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Conservative
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A; Molecule type: DNA
Msesidues: 1-431 AEMNA
A; Residues: 1-431 AEMNA
A; Residues: 1-431 AEMNA
A; Residues: 1-431 AEMNA
A; Cross-references: UNIPPOT: PS4074; EMBL: Z49702; NID: 9817859; PID: 91326013; GSPDB: GN00013:
A; Experimental source: strain AB972
A; Experimental source: strain AB972
B; Experimental source: strain AB972
B; Experimental source: strain AB973
B; Experimental source: strain AB973
B; Experimental source: S54014
A; Reference number: S54014
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C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Tae.Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C.Accession: T18975
B.McMurray, A.
Submitted to the EMBL Data Library, June 1995
A.Rccession: T18975
A.Rccession: T18975
A.Rccession: T18975
A.Rccession: T18975
A.Rccession: T18976
A.Rccessi
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A,Moceaule type: DNA
A,Moceaule type: DNA
A,Cross-references: 345-624 <LyEs
A,Cross-references: BMBL:249273; NID:g809577; PID:g809578; GSPDB:GN00013; MIPS:YMR119w
C,Generics:
A,Map Dosition: 13R
C,Superfamily: probable membrane protein YMR119w
C,Reywords: transmembrane protein
F;82-98/Domain: transmembrane #status predicted <TM1>
F;120-136/Domain: transmembrane #status predicted <TM2>
F;211-227/Domain: transmembrane #status predicted <TM4>
F;211-227/Domain: transmembrane #status predicted <TM4>
F;218-294/Domain: transmembrane #status predicted <TM4>
F;278-294/Domain: transmembrane #status predicted <TM5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable membrane protein YMR119w - yeast (Saccharomyces cerevisiae)
NyAlternate names: hypothetical protein YM8564.01; hypothetical protein YM9718.18
C,Species: Saccharomyces cerevisiae
C,Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C,Accession: S54581; S54488
Submitted to the EMBL Data Library, May 1995
A,Reference number: S54510
                                                      F,42-68/Domain: Bowman-Birk inhibitor repeat homology <BB1>
F;69-94/Domain: Bowman-Birk inhibitor repeat homology <BB2>
F;41-95,42-57,45-91,47-55,65-72,69-84,74-82/Disulfide bonds: #status predicted F;49/Inhibitory site: Ala (elastase) #status predicted F;76/Inhibitory site: Arg (trypsin) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                         Length 103;
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43.1%; Score 50; DB 1; Length 624;
Best Local Similarity 42.3%; Pred. No. 39;
Matches 11; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                  43.5%; Score 50.5; D
58.8%; Pred. No. 10;
tive 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 58.8%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: S54581
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Cispecies: Glycine max (soybean)
Cipate: 24.Apr-1994 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
CiAccession: A25666, A01302
CiAccession: A25666, A01302
CiAccession: Chem. 259, 9883-9880, 1984
A.Title: Molecular cloning and analysis of a gene coding for the Bowman-Birk protease in A;Reference number: A92469; MUID:84264652; PMID:6086657
A;Contents: annotation
A;Acontents: annotation
A;Acontents: annotation
A;Acontents cannotation
A;Acontents cannotation
A;Acontents cannotation
A;Acontents: as a content a co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bowman-Birk proteinase isoinhibitor C-II precursor (clone pB24) - soybean C. Specides: Glycine max (soybean) C. Specides: Glycine max (soybean) C. Date: 28-Aug-1985 #sequence_revision 07-oct-1994 #text_change 18-Aug-2000 C; Accession: JC2225 R; Baek, J.M.; Song, J.C.; Choi, Y.D.; Kim, S.I. Biosci. Biotechnol. Biotechnol. Biotechnol. Biotechnol. Biotechnol. Biotechnol. Biotechnol. Biotechnol. Siochem. 58, 843-846, 1994 A; Title: Nuclectide sequence homology of CDNAs encoding soybean Bowman-Birk type protein A; Reference number: JC2224; MUID: 94289861; PMID: 7764974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-94 <BAE>
C;Comment: This protein regulates endogeneous proteinase during germination, stores sulf
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Accession. 122638.
A,Molecule type: DNA
A,Residues: 1-103 <HAN>
A,Residues: 1-103 <HAN>
A,Crose_references: UNIPROT: P01063, GB:K01967; NID:g169942; PIDN:AAA33952.1; PID:g169943
R;Odani, S., Ibenaew, T.
J: Biochem. 82, 1523-1531, 1977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R.Odani, S.; Ikenaka, T.
J. Biochem. 82, 1523-1531, 1977
J.Reference number: A01302, MUID:78087480; PMID:599141
A.Accession: A01302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A; Residues: 28-103 < CODA.
C; Comment: This protein inhibits trypsin, elastase, and chymotrypsin. The site of intera
C; Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
C; Ksywords: duplication; seed; serine proteinase inhibitor
F;1-27/Domain: signal sequence #status predicted < SIG>
F;28-103/Product: proteinase inhibitor (Bowman-Birk) C-II #status experimental < MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Keywords: duplication; seed; serine proteinase inhibitor
F;1-18/Domain: signal sequence #status predicted <51G>
F;1-9-94/Product: Bowman-Birk proteinase isoinhibitor C-II #status predicted <MAT>
F;33-59/Domain: Bowman-Birk inhibitor repeat homology <BB1>
F;60-85/Domain: Bowman-Birk inhibitor repeat homology <BB12>
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                     'n
                                                      43.5%; Score 50.5; DB 2; Length 83; 58.8%; Pred. No. 9.6; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 43.5%; Score 50.5; DB 2; Length 94; Local Similarity 58.8%; Pred. No. 9.4; ss 10; Conservative 1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                  51 RCACTRSMPGOCRCLDT 67
                                                                                                                                                                                                                                                                                            4 RCICTR---GFCRCICT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 RCICTR---GFCRCICT 17
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A; Start codon: GTT
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Matches
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A;Gene: CESP:C06A1.6 A;Map position: 2 A;Introns: 22/3

1 GFCRCICTRGFCRCIC 16

82

67 GGCGCCCRPRCCCC

thyroglobulin - rat (fragments)

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Directinase inhibitor (Bowman-Birk) II - kidney bean (tentative sequence)
C;Species: Phaseolus vulgaris (kidney bean)
C;Date: 30-Nov-1880 #sequence_revision 30-Nov-1980 #text_change 09-Jul-2004
C;Accession: A01299
R;Wilson, K.A.; Laskowski Sr., M.
J. Biol. Chem. 250, 4261-4267, 1975
A;Title: The partial amino acid sequence of trypsin inhibitor II from garden bean, Phasec A;Reference number: A01299; MUID:75151596; PMID:1126951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C,Accession: A01300
R;Kiyohara, T.; Yokota, K.; Masaki, Y.; Matsui, O.; Iwasaki, T.; Yoshikawa, M.
R;Kiyohara, T.; Yokota, K.; Masaki, Y.; Matsui, O.; Iwasaki, T.; Yoshikawa, M.
B;Chem. 90, 721-728, 1981
A;Title: The amino acid sequences of proteinase inhibitors I-A and I-A' from adzuki beans
A;Reference number: A01300; MUID:82075699; PMID:7309695
                                                                Cipate: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
Cjacession: G01300, A01300
R;Kiyohara, T.; Yokota, K.; Masaki, Y.; Matsui, O.; Iwasaki, T.; Yoshikawa, M.
Biochem. 90, 721-728, 1981
A;Title: The amino acid sequences of proteinase inhibitors I-A and I-A' from adzuki beans
A;Reference number: A01300; MUID:82075699; PMID:7309695
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C;Comment: This inhibitor strongly inhibits trypsin.
C;Comment: This inhibitor strongly inhibitor; Bowman-Birk inhibitor repeat homology C;Superfamily: Bowman-Birk proteinase inhibitor c;Keywords: duplication; serine proteinase inhibitor p;19-45/Domain: Bowman-Birk inhibitor repeat homology <BB1>
F;46-71/Domain: Bowman-Birk inhibitor repeat homology <BB2>
F;18-72,19-34,22-68,24-32,42-49,46-61,51-59/Disulfide bonds: #status predicted F;53/Inhibitory site: Lys (trypsin) #status experimental F;53/Inhibitory site: Arg (trypsin) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inhibitor repeat homology
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A,Molecule type: protein
A,Racessidues: 1-72 <KIY2
A,Racessidues: 1-72 <KIY2
A,Cross-references: UNIPROT:P01061
C,Comment: This inhibitor strongly inhibits trypsin.
C,Superfamily: Bowman-Birk proteinase inhibitors; Bowman-Birk inhibitor repeat homology <BB1>
F,40-65/Domain: Bowman-Birk inhibitor repeat homology <BB1>
F,12-66,13-28,1662,18-26,36-413,40-55,45-53/Disulfide bonds: #status predicted
F,20/Inhibitory site: Lys (trypsin) #status predicted
F,47/Inhibitory site: Arg (trypsin) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C, Species: Vigna angularis (adzuki bean)
C, Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.4%; Score 48; DB 1; Length 78; 52.6%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 48; DB 1; Length 72;
Pred. No. 15;
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- adzuki bean
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C:Species: Vigna angularis (adzuki bean)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 52.6%; Pred. No. 15;
Matches 10; Conservative 3; Mismatches
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                                                          bean)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CKSCMCTRSMPGQCRCLDT
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A,Molecule type: protein
A,Residues: 1-78 <KIY>
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Best Local Similarity
Matches 10; Conserv
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C;Species: Chironomus tentans
C;Species: Chironomus tentans
C;Species: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Aug-2004
C;Accession. 508167
R;Paulsson, G; Lendahl, U; Galli, J; Ericsson, C; Wieslander, L.
C;Accession. 508167
Mol. Biol. 21, 331-349, 1990
A;Title: The balbiani ring 3 gene in Chironomus tentans has a diverged repetitive struct A;Reference number: 808167
My.Reference number: 808167
A;Reference number: 808167
A;Recession: 508167
A;Recession: 508167
A;Recession: 508167
A;Recession: 508167
A;Residues: 1-1700 PAU>
A;Res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Decises attus norvegicus (Norway rat)
C; Date: 20-Unu-1999 #sequence_revision 30-Jun-1991 #text_change 11-Apr-1997
C; MacCossion: A25964
A; Millor (20-MacCossion A25964)
A; Molecule type: DNA
A; Molecule ty
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                                                                                                                                                                                                                              Query Match
42.2%; Score 49; DB 2; Length 152;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 8; Indels
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g

Query Match

Best Loc Matches

RESULT 17 TIZB1P

3 CRCICTRG---

---FCRCIC 16

42.2%;

Query Match
Best Local Similarity 23.3
Matches 7; Conservative

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A;Molecule type: protein
C;Comen: 267, 1990-1994, 1992
A;Citle: Reactive sites of an anticarcinogenic Bowman-Birk proteinase inhibitor are simil
A;Reference number: A42052; MUD: 92112932; PMID: 1730/7010
A;Reference number: A42052; MUD: 92112932; PMID: 1730/700 PI - II at 2.5 angstroms
C;Comment: This protein xerglates endogeneous proteinase during germination, stores sulf,
C;Reywords: duplication; Seed; serine proteinase inhibitor; storage protein
F;1287/Domain: signal sequence #status predicted <SIG>F;28-102/Product: proteinase inhibitor (Bowman-Birk inhibitor repeat homology <BB1>F;1-96/Domain: Bowman-Birk inhibitor repeat homology <BB2>F;4-70/Domain: Bowman-Birk inhibitor repeat homology <BB2>F;4-39/4-59,49-57,67-74,186,76-84/Disulfide bonds: #status experimental
F;1/Inhibitory site: Arg (trypsin) #status predicted
F;78/Inhibitory site: Arg (trypsin) #status predicted
                         A, Experimental source: clone pB26
R; Odani, S.; Ikenaka, T.
Biochem. 83, 737-745, 1978
A; Title: Studies on soybean trypsin inhibitors. XII. Linear sequences of two soybean dout A, Reference number: A01303; MUID: 78150870; PMID: 641033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-160 <WIL>
A;Cross-references: UNIPROT:Q9XU68; EMBL:Z83127; PIDN:CAB05630.1; GSPDB:GN00022; CESP:T2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S32834
methylviologen-reducing hydrogenase chain vhcG [similarity] - Methanococcus voltae C;Species: Methanococcus voltae C;Species: Methanococcus voltae C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004 C;Accession: S32834; S16726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein T23F6.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Decies: Caenorhabditis elegans
C;Decession: T25185
R;Lloyd, C.
Submitted to the EMBL Data Library, November 1996
A; Cross-references: EMBL: X68706; NID: 918571; PIDN: CAA48657.1; PID: 918572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4,
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8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48; DB 1; Length 102;
Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: Z19992
A;Accession: T25185
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 48; DB 2;
Pred. No. 27;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 CKCCOPVCTNACTNGGGCSCGCTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 CR-CICTR---GFCRCICT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.4%;
52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: clone T23F6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.4%;
Local Similarity 41.7%;
Les 10; Conservative ;
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                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 28-102 <001>
A;Accession: B01303
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A;Gene: CESP:T23F6.1
                                                                                                                                                                                                                 A; Accession: A01303
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                         A;Cross-references: UNIPROT:P01060
A;Cross-references: UNIPROT:P01060
A;Note: two forms of the inhibitor were isolated; the amino end of the longer form is black.
A;Note: two forms of the inhibitor were form
C;Comment: This protein inhibits elastese and trypsin simultaneously and independently.
C;Comment: This protein inhibits elastese and trypsin simultaneously and independently.
C;Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology will blocked amino end; duplication; serine proteinase inhibitor
F;18-44/Domain: Bowman-Birk inhibitor repeat homology will be proteined inhibitor repeat homology will be proteined.
F;17-71,18-33,21-67,23-141.48,45-60,50-58/Disulfide bonds: #status predicted
F;25/Inhibitory site: Ala (trypsin) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Andreaduses: 1-102 c8ON>
(Ross-references: UNIPROT:043709; EMBL:X68707; NID:9288618; PIDN:CAA48658.1; PID:92886
(Back, JM.; Song, J.C.; Chol., Y.D.; Kim, S.I.
(Soci. Biotechnol. Biochem. 58, 84-3-846, 1994
(Title: Nucleotide sequence homology of cDMAs encoding soybean Bowman-Birk type protein; Reference number: JC2224; MUID:94289861; PMID:7764974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P01064; EMBL:M20733; NID:g169946; PIDN:AAA33954.1; PID:g1699
C;Superfamily: Bowman-Birk proteinase inhibitor: Bowman-Birk inhibitor repeat homology
F;25-51/Pomain: Bowman-Birk inhibitor repeat homology <BBL>
F;52-77/Pomain: Bowman-Birk inhibitor repeat homology <BBL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteinase inhibitor (Bowman-Birk) D-II precursor - soybean
N;Contains: proteinase inhibitor (Bowman-Birk) E-I (PI-II)
C;Species: Glycine max (soybean)
C;Species: Glycine max (soybean)
C;Accession: 53243, 402224; A01303; 829559
K;Song, U.C.; Back, U.M.; Kim, S.I.
submitted to the EMBL Data Library, October 1992
A;Reference number: 532243
A;Reference number: 532243
A;Accession: 532343
A;Accession: 532343
A;Accession: S32343
A;Accession: S3243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteinase inhibitor IV - soybean
C;Species: Glycine max (soybean)
C;Date: 02-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C;Accession: 807941
R;Joudrier, P.E.; Foard, D.E.; Floener, L.A.; Larkins, B.A.
Plant Mol. Biol. 10, 35-42, 1987
A;Title: Isolation and sequence of cDNA encoding the soybean protease inhibitors PI IV is a februaries.
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Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.4%; Score 48; DB 2; Length 83; 52.6%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
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52 CKSCMCTRSQPGQCRCLDT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 52.6%;
Matches 10; Conservative
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Matches 10; Conservative
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A;Molecule type: mRNA
A;Residues: 1-83 <JOU>
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5

Gaps

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C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JH6675; PS0385; S23254
R;Noerenberg, U.; Wille, H.; Wolff, J.M.; Frank, R.; Rathjen, F.G.
Nauron B, 849-863, 1992
A;Title: The chicken neural extracellular matrix molecule restrictin: similarity with EGI
A;Accession: JH0675; MUID:92265298; PMID:1375037
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C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 148725
R:Wagner, S.; Cullmarn, G.; Knippers, R.
A; Virol. 65, 3259-3267, 1991
A;Title: The Q300 game: a novel transcription unit induced in simian virus 40-infected ar
A;Reference number: 148725; MUID:91237845; PMID:1851876
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Roses: 1-77 <RES>
A;Cross-references: UNIPROT:Q02722; EMBL:X52164; NID:g53860; PIDN:CAA36417.1; PID:g53861
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46.7%; Pred. No. 19;
tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 CRCICSEGWAGSNCS 199
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Best Local Similarity 46.74
Matches 7; Conservative
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Query Match
Best Local Similarity 46.71
Matches 7; Conservative
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Cisuperfamily: vertebrate rhodopain

Cisuperfamily: vertebrate rhodopain

Cisuperfamily: vertebrate rhodopain

Fig. 1977/Domain: transmembrane #status predicted <TM2>

Fig. 107-129/Domain: transmembrane #status predicted <TM3>

Fig. 107-129/Domain: transmembrane #status predicted <TM3>

Fig. 107-129/Domain: transmembrane #status predicted <TM4>

Fig. 199-222/Domain: transmembrane #status predicted <TM4>

Fig. 199-222/Domain: transmembrane #status predicted <TM6>

Fig. 109-222/Domain: transmembrane #status predicted <TM6>

Fig. 109-128/Domain: transmembrane #status predicted <TM7>

Fig. 109-109/Domain: transmembrane #statu
                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: UNIPROT:Q00406; EMBL:X61203; NID:g296614; PIDN:CAA43505.1; PID:g2966
R;Halboth, S.; Klein, A.
Submitted to the EMBL Data Library, August 1991
A;Description: Methanococcus voltae harbors two gene groups each of homologous (NiPe) - a
A;Reference number: S16721
A;Accession: S16726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Halboth, S.; Klein, A.
Mol. Gen. Genet. 233, 217-224, 1992
A;Fitle: Methancoccus voltae harbors four gene clusters potentially encoding two [NiFe]
A;Feference number: A59304; MUID:92293118; PMID:1603063
A;Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: JC5042
R;Isoai, A.; Kawahara, H.; Okazaki, Y.; Shizuri, Y.
Gene 175, 95-100, 1996
A;Title: Molecular cloning of a new member of the putative G protein-coupled receptor ge A;Reference number: JC5042; MUID:97074655; PMID:8917082
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A;Residues: 1-476 <ISO>
A;Cross-references: UNIPROT:Q93126; DDBJ:D78363; NID:g1514430; PIDN:BAA11375.1; PID:g151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Molecule type: DNA
A,Residues: 1-99,'TA',102-107,'P',126,'LH',129-306 <HAL>
A,Cross-references: EMBL:X61203
A,Note: the sequence is revised in Genbank entry X61203, release 117, (PIDN:CAA43505.1)
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C,Species: Balanus amphitrite (barnacle)
C,Date: 21-Jan-1997 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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C,Superfamily: methyl viologen-reducing hydrogenase gamma chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 48; DB Pred. No. 41; 1; Mismatches
R;Klein, A.
submitted to the EMBL Data Library, August 1991
A;Reference number: 832833
AAcceseion: 832834
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Query Match
Best Local Similarity 50.0%;
Matches 7; Conservative

g

Accession: JC5042

RESULT 25

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Query Match

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GB:AF219993
transmembrane protein on cell surface with an antiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;31-50/Domain: transmembrane #status predicted <TMM>
F;255-317/Region: conserved carboxyl-terminus, homologous to chondromodulin-I #status pre
F;265-306/Domain: antiangiogenic #status predicted <ANT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: CESP:F46C8.4
A;Introns: 19/3; 61/3; 80/1; 159/1; 182/1; 208/2; 246/1; 308/1; 367/1; 422/1; 466/1; 507/
629/3; 1721/3; 1767/3; 1811/1; 1874/1; 1920/1; 2011/2; 2068/3; 2117/1; 2161/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. Blophys. Res. Commun. 280, 1323-1327, 2001
A; Title: Molecular cloning of tenomodulin, a novel chondromodulin-I related gene.
A; Reference number: JC7603; MUID:21092761; PMID:11162673
A; Contents: Embryo, 17-days
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004 C;Accession: JC7603 R;Shukunami, C.; Oshima, Y.; Hiraki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein F46C8.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                        Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 317;
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A;Cross.references: EMBL:U41624; PIDN:AAA83316.1; CESP:F46C8.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                       A;Map position: Xq22
C;Keywords: transmembrane protein
F;31-50/Domain: transmembrane #status predicted <TVM>
F;265-317/Region: highly conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      core 47; DB 2;
red. No. 55;
Mismatches 5
                                                                                                                                                                     Score 47; DB 2;
Pred. No. 55;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                  263 GYCCIYCRRGNRYCRRVC 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 GYCCIYCRRGNRYCRRVC 280
                                                                                                                                                                                                                                                                                1 GFCRCICTRG--FCRCIC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Molecule type: mRNA
A Residues: 1.317 < SHU>
A)Cross-references: URPROT: Q9EP64;
C)Comment: Tenomodulin is a type II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GPCRCICTRG--FCRCIC 16
                                                                                                                                                    Query Match
Best Local Similarity 44.4%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 44.4#
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: T34264
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A;Gene:
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                                                        Nighternate names: ORFia protein
C;Species: lactic dehydrogenase virus
C;Date: 3.1-Dec-1933 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: P00618
R;Chen, Z.; Kuo, L.; Rowland, R.R.R.; Even, C.; Faaberg, K.S.; Plagemann, P.G.W.
J. Gen. Virol. 74, 643-660, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Molecule type: mRNA
A, Residues: 1-113 <MCG>
A, Cross-references: UNPROT:Q40330; EMBL:X79880; NID:g509373; PIDN:CAA56254.1; PID:g5093
A, Cross-references: UNPROT:Q40330; EMBL:X79880; NID:g509373; PIDN:CAA56254.1; PID:g5093
C, Superfamily: Bowman-Birk proteinase inhibitor
C, Keywords: serine proteinase inhibitor
F;56-113/Product: trypsin inhibitor #status predicted <MAT>
F;60-85/Domain: Bowman-Birk inhibitor repeat homology <BB1>
F;86-111/Domain: Bowman-Birk inhibitor repeat homology <BB1>
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A.Title: Molecular cloning and characterization of ChMIL, a novel member molecule simila A.Reference number: JC7597; MUID:21092728; PMID:11162640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Cross-references: UNIPROT:09H2S6
;Comment: This protein is a novel type II transmembrane protein which is similar to chd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AII) cDNAs from alfalfa leaves
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Urypsin inhibitor precursor (clone ATI21) - alfalfa
Nylternate names: serine proteinase inhibitor
(Species: Medicago sativa (alfalfa)
(Spacies: Medicago sativa (alfalfa)
(Spaces: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
(Spacession: S5648; S491180 = x87 knh, N.; Ryan, C.A.
R;McGurl, B.; Mukherjee, S.; Kahn, N.; Ryan, C.A.
Plant Mol. Biol. 27, 995-1001, 1995
A;Title: Characterization of two proteinase inhibitor (ATI) cDNAs from alfalaxeterine number: S56647; MUID:95284355; PMID:7766888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.Species: Homo sapiens (man)
C.Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C.Accession: JC7597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 550;
                                   lypothetical protein 550 - lactic dehydrogenase virus (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 113;
                                                                                                                                                                                                                                                                                      A, Reference number: JQ1990; MUID:93224885; PMID:8385693
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7
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Pred. No. 28;
2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.4%; Pred. w.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 47.5;
Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 GFDRCLCTPWAKVFWERGQVYCTRCLAAR 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GFCRCICT-----RG--FC-RCICTR 18
                                                                                                                                                                                                                                                                                                                 A, Accession: PQ0618
A, Molecule type: mRNA
A, Residues: 1-550 CHEA
A, Exosareferences: UNIPROT: 083017; GB: L06812
A, Experimental source: isolate P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chondromodulin-I like protein, ChMIL - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 ČKSCICTRSYPPOCRC 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 41.43
Matches 12; Conservative
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Best Local Similarity
Matches 9; Conserv
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A; Residues: 1-317 < YAM>
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A)Residues: 1-4660 (SAI>
A)Residues: 1-4660 (SAI>
A)Cross-references: UNIPROT: P98158; EMBL: L34049; NID: 9561852; PID: 9561853; PIDN: AAA51369.
A)Cross-references: UNIPROT: P98158; EMBL: L34049; Kidney
C; Experimental Source: strain Sprague-Dawley; Kidney
C; Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding
F; 1-25/Domain: signal sequence #status predicted <SIG>
F; 26-4660/Product: 9p330 protein #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C'Accession: T49781 F. R. Fartmann, B.; Holland, R.; Nyakatura, Submitted to the Protein Sequence Database, May 2000 A;Reference number: 225022
         Cypecies: Nattus norvegicus (Norway rat)
Cybecies: Nattus norvegicus (Norway rat)
Cybecies: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
CyAccession: T42737
Fysito, A.; Pietromonaco, S.; Loo, A.K.C.; Farquhar, M.G.
Proc. Natl. Acad. Sci. U.S.A. 91, 9725-9729, 1994
A,Title: Complete cloning and sequencing of rat gp330/megalin, a distinctive member of A,Recession: T47737
A,Rocession: T47737
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Rocession: A,Roce
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-883-62(2)-84,62(2)-84,62(2)-84,62(2)-84,62(2)-84,63(2)-84,63(2)-84,63(2)-84,63(2)-84,63(2)-84,63(2)-84,63(2)-84,63(2)-84,63(2)-84,63(2)-84,63(2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein H23N18.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T33883
R;Courtney, L.; Langston, L.; Maupin, R.
submitted to the RML Data Library, February 1999
A;Description: The sequence of C. elegans cosmid H23N18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               related to mutanase (mutA) gene [imported] - Neurospora crassa
NA-Alternate names: protein B9110.180
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 40.5%; Score 47; DB 2; Length 4660; Best Local Similarity 50.0%; Pred. No. 3.4e+02; Matches 9; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 RNVCDEGFCKCAKNAAKSLPLCT 121
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Matches 8; Conservative
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A; Map position: 5
A; Introns: 33/2; 80/1; 121/3
    N;Alternate names: megalin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-141 <COU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: T33983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 36
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A,Introns: 18/1, 73/2, 101/3, 241/2, 251/1, 327/3, 383/3, 455/3, 494/1, 793/1, 905/3, 1d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ajŝtatus: preliminary; translated from GB/EMBL/DDBJ
AjMoLecule type: DNA
Ajsesidues: 1.2946 < cDUZs
AjCross-references: EMBL:U40410; NID:gl065453; PID:gl065455; PIDN:AAA81392.1; CESP:C54G7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: CESP:C54G7.3
A;Introns: 16/1; 53/2; 92/1; 160/3; 295/1; 346/1; 392/1; 440/1; 475/3; 579/1; 615/3; 169
46/1; 2561/2; 2603/2; 2626/2; 2665/2; 2716/3; 2804/3; 2884/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-3191 <WIL>
A;Cross-references: UNIPROT:001335; EMBL:281094; PIDN:CAB03155.1; GSPDB:GN00023; CESP:TC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'n
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A;Residues: 1-3191 - 4WI2.
A;Cross-references: EMBL;Z81110; PIDN:CAB03261.1; GSPDB:GN00023; CESP:T01D3.1
A;Experimental source: clone T01D3
                                                                                                                                                                                                 hypothetical protein C54G7.3 - Caenorhabditis elegans
C.Speciese: Caenorhabditis elegans
C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C.Accession: T15840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein T01D3.1 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C:Date: 15-OGC-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22945; T24295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.5%; Score 47; DB 2; Length 2946; 66.7%; Pred. No. 2.5e+02; tive 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                   R,Du, Z.
submitted to the EWBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid C54G7.
A;Reference number: Z18416
A;Reference: T15840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1182 GLCKCEDGWQGSRCQIPLCNSCSLNGICTRPGFCSC 1217
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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submitted to the EMBL Data Library, October 1996
A;Reference number: Z19870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RiPercy, C. submitted to the EMBL Data Library, October 1996 A;Reference number: Z19640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Experimental source: clone F58G11
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T42737
gp330 protein precursor - rat
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2430 VCTNGFCHC 2438
1215 VCVNGFCRC 1223
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Best Local Similarity
Matches 11; Conserv
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C;Genetics: A;Gene: NCSP:B9J10.180 A; Introns: 26/3; 198/1

A; Map position: 6

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112 CKSCMCTRSMPGKCRCL 128

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us-10-009-317a-32.rpr

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Superfamily: human hypothetical protein DBCCR1
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Job time : 33.5 secs
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ilarity 50.0%;
Conservative 1
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Best Local Similarity 53.8°
"" 7; Conservative
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Best Local Similarity
7, Conserve
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                                                                                                                                                                                                                                                                                                           reelin precursor - mouse

C;Species: Mus musculus (house mouse)

C;Accession: S58870; S71844; I49297

R;D'Arcangelo, G; Miao, G.G.; Chen, S.C.; Soares, H.D.; Morgan, J.I.; Curzan, T.

Asture 374, 719-723, 1995

A;Title: A protein related to extracellular matrix proteins deleted in the mouse mutant

A;Reference number: I49297; MUID:95231649; PMID:7715726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: S09415
R;Hilder, V.A.; Barker, R.F.; Samour, R.A.; Gatehouse, A.M.R.; Gatehouse, J.A.; Boulter, Plant Mol. Biol. 13, 701-710, 1989
A;Titler: Protein and cDNA sequences of Bowman-Birk protease inhibitors from the cowpea (A;Reference number: S09414; MUID:91370854; PMID:2491685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-146 < HIL>
C;Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
C;Superfamily: Bowman-Birk inhibitor repeat homology <BB1>
F;85-111/Domain: Bowman-Birk inhibitor repeat homology <BB2>
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A; Cross-references: EMBL:U24703; NID:g902486; PID:g902487
E;1-27/Domain: signal sequence #status predicted <SIG>
E;28-3461/Product: reelin #status predicted <MAT>
F;18-3461/Product: reelin #status predicted <MAT>
F;1769-1795/Domain: EGF homology <EGF>
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C:Species: Vigna unguiculata (cowpea)
C:Date: 21-Nov-1993 #sequence_revision 21-Jul-1995 #text_change 23-May-1997
                                                                                            Gaps
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40.1%; Score 46.5; DB 2; Length 3461;
Best Local Similarity 47.4%; Pred. No. 3.2e+02;
Matches 9; Conservative 1; Mismatches 6; Indels 3;
                                        Length 883;
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                                                                                    8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A Status: nucleic acid sequence not shown
A, Molecule type: mRNA
A, Residues: 1-3461 - 6DAR>
A; Cross-references: EMBL:U24703; NID:g902486; PID:g902487
Submitted to the EMBL bata Library, April 1995
A; Reference number: 871844
                           40.1%; Score 46.5; DB 2;
45.0%; Pred. No. 1.3e+02;
1ve 0; Mismatches 8;
                                                                                                                                                                                   556 GLČSFSČNFGFČPIHSČTČT 575
                                                                                                                                1 GFCRCICTRGFC---RCICT 17
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                                                                                 Conservative
Query Match
Best Local Similarity
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Molecule type: mRNA
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A;Molecule type: mRNA
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C;Accession: T09052
F;Alabuchi, T.; Luscombe, M.; Elder, P.A.; Knowles, M.A.
Genomics 48, 277-288, 1998
A;Title: Structure and methylation-based silencing of a gene (DBCCRI) within a candidate A;Reference number: Z16537; MUID:98207242; PMID:9545632
A;Ceession: T09052
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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A,Cross-references: UNIPROT.060477; EMBL:AF027734; NID:g3041876; PIDN:AAC39691.1; PID:g3(
A,Experimental source: tissue type: brain; developmental stage: fetal and infant
hypothetical protein DKF2pS86M2123.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T17298
R;Ansorge, W.; Wirkner, U; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
Bubmitted to the Protein Sequence Database, September 1999
A;Reference number: Z18729
A;Reference number: Z18729
A;Reference preliminary
A;Reference Hype: mRNA
A;Residues: 1-511 < ANS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein DBCCR1 - human
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
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Pred. No. 1.3e+02;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q9NS15; EMBL:AL117551
A;Experimental source: adult uterus; clone DKFZp586M2123
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89 76.7 18 8 8 75.9 18 5 8 75.0 18 5	1 87 75.0 18 6 8 7 75.0 18 8	3 86 74.1 18 5 86 74.1 18 5 74.1 18 5	37 86 74.1 18 8 ADO35.3 38 85 73.3 18 6 AAE331 39 85 73.3 18 6 AAE331 50 65 73.3 18 8 ADO35.3	1 85 73.3 18 8 85 73.3 18 8 8 8 73.3 18 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	71.6 19 8 71.6 18 8 71.6 18 8		AL.	RESULT 1 AAB35046 ID AAB35046 standard, peptide, 18 AA	AX AAB35046;	DT 27-MAR-2001 (first entry) XX DE Theta defensin SEQ ID NO: 30.	XX KW Theta defensin; antimicrobial; cy KW virus; helminth; disinfectant; fo	os Unidentified.	XX PN WO200068265-A1. XX	16-NOV-2000.	PF 10-MAY-2000; 2000WO-US012842.	PR 10-MAY-1999; 99US-00309487.	(REGC) UNIV CALIFORNIA.	PI Selsted ME, Tang Y, Yuan J, Ou	DR WPI; 2001-031853/04.	Pr Novel theta defensin peptide with	######################################			bacterial, disinfectar	XX SQ Sequence 18 AA;	Query Match 100.0%; Sco	18; Conservative 0;	Qy 1 GECRCICTRGFCRCICTR 18	Db 1 GFCRCICTRGFCRCICTR 18
5.1.6 Compugen Ltd.		. Search time 115 Seconds (without alignments) 56.149 Million cell updates/sec			W	rs: 2002273							<pre>cted by chance to have a of the result being printed, score distribution.</pre>) }		Description	Thet	Adc35230 Rhesus th	Anti-vi	Abb53297 Mari-vira	Add95202 (Yellic de	Add35357 Antimicro Adg70012 Rhesus th	Rhesus Rhesus		Ado35263 Monkey RT Ado35255 Rhesus th	12Y re Illy r	Adnoslso Human rec Adnoslsi Human ret Aabsoog Bhasse ma	Addison American Appelson Appe	Aae33801 Human rec Aae33863 Enantio-r
GenCore version 5.1 Copyright (c) 1993 - 2004 Con	protein search, using sw model	October 26, 2004, 15:13:05 ; Sec (with	US-10-009-317A-32 116 1 GFCRCICTRGFCRCICTR 18	BLOSUM62 Gapop 10.0 , Gapext 0.5	2002273 seqs, 358729299 residues	hits satisfying chosen parameter	length: 0 length: 200000000	Minimum Match 0% Maximum Match 100% Listing first 45 summaries	A_Genes		5: geneseqp2002s:* 6: geneseqp2003as:* 7: geneseqp2003bs:*	: geneseqp2004s	. is the number of results predicted by eater than or equal to the score of the orived by analysis of the total score d	SUMMARIES		Query Match Length DB ID	100.0 18 4	1000.0	88.8 18 5	87.1 18 5	87.1 18 5	87.1 18 8 87.1 18 8	87.1 18 8 87.1 18 8	87,1 18 8 ADO35239 87,1 18 8 ADO35250	87.1 38 8 86.2 18 8	80.2 18 6 80.2 18 6	80.2 18 8	77.6 18 5	77.6 18 6
	OM protein - pro	Run on:	Title: Perfect score: Sequence:	Scoring table:	Searched:	Total number of	Minimum DB seq Maximum DB seq	Post-processing	Database :				Pred. No. score gre	n -		Result No. Score	!			,,,,		0 -	2.6	14 101	9 6	മ ക	0 -1 0	N m •	4.1

'n	Ado35249 Rhesus th	Abp53298 Anti-vira	Aau91017 Transplan	Aae33864 Enantio-R	Aae33802 R9K retro	7 Human	Aab35047 Theta def		231 Rhesus	242 Rhesus	Ado35241 Rhesus th	Aae33804 I15Y retr	Aae33803 I6Y retro	Ado35256 Rhesus th	Adn08179 Human ret	Adn08178 Human ret	L)	Ado35246 Rhesus th	Ado35245 Rhesus th
8 ADN08176	8 ADO35249	5 ABP53298	5 AAU91017	6 AAE33864	6 AAE33802	8 ADN08177	4 AAB35047	5 ABP53296	8 AD035231	8 AD035242	8 ADO35241	6 AAE33804		8 AD035256	8 ADN08179	8 ADN08178	6 AAE33807	8 ADO35246	8 ADO35245
18	18	18	18	18	178	78	78	18	18	18	18	18	18	18	18	18	18	18	18
77.6	76.7		75.0			75.0	74.1	4	74.1	74.1			73.3						71.6
06	68	8	87	87		87													83
26	27	e c	60	0.6		3.5		3.4	35				9 69 9 69			42	4.3		4.5

ALIGNMENTS

0; ion provides theta defensin peptides and analogues robial activity. They can be used in the treatment of fungal, protozoan and helminthic infections, in as food preservatives Gaps imicrobial; cyclic; bacterium; fungus; protozoan; sinfectant; food preservative; analogue. in peptide with antimicrobial activity against ingi, protozoa and viruses. 0; 100.0%; Score 116; DB 4; Length 18; 100.0%; Pred. No. 8.1e-06; varive 0; Mismatches 0; Indels , Yuan J, Ouellette AJ; peptide; 18 AA. .10pp; English. ID NO: 30. -US012842. -00309487. entry) RNIA.

Monkey, Rhesus theta defensin, RTD-2; antimicrobial peptide; cyclic, antimicrobial; antinflammatory; antibacterial; virucide; fungicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial infection, viral infection; disinfectant; fungal infection; haemolytic activity.

Rhesus theta defensin peptide, RTD-2.

(first entry)

15-JUL-2004

AD035230;

Ā

AD035230 standard; peptide; 18

RESULT 3 AD035230

38

GFCRCICTRGFCRCICTR

18
 7nte= "The peptide is cyclised by a covalent link between these two residues"

Location/Qualifiers

Macaca mulatta. Key Modified-site

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RESULT

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Ouery Match
100.0%; Score 116; DB 5;
Best Local Similarity 100.0%; Pred. No. 8.1e-06;
Matches 18; Conservative 0; Mismatches 0;
                                               WO200260468-A2.
                                                                                                                                                                                             Sequence 18 AA;
                                      Macaca mulatta
              13-NOV-2002
                                                     38-AUG-2002
                                         Synthetic.
ABP53295
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The present invention describes a method (M1) of using a first anti-viral peptide (I) comprising a theta-defensin peptide in an amphipathic alphabelious structure in a lipid environment for reducing the infectivity of a virus. (I) can have virucide and anti-HIV activities, and can be used to reduce virus growth, infectivity burden, shed, and development of anti-viral resistance. (I) can be used for inhibiting the growth and proliferation of a virus and so can be used for; (a) protecting or treating subject form a viral infection, preventing recurrent viral infection in a subject harbouring a latent virus, controlling virus in subject harbouring a latent virus, controlling virus shed from a VS. reducing percentage of VS in a contaminated within a virally-infected subject (VS), reducing virus latency in a VS, reducing virus shed from a VS. reducing percentage of VS in a contaminated tissue or fluid sample safe for use, or reducing the number of population regardless of virus; infection of viruses. (M1) is useful for infectious virus particles in a population of viruses, waire, cars, fowl and humans e.g. an enveloped virus infecting humans such as human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is administered to a patient who is immunosuppressed or to a subject who is cont infected with the virus, where the first anti-viral peptide is administered to a patient who is immunosuppressed to a patient who is immunosuppressed to a subject who is continity infected with the virus, where the first anti-viral peptide is administered by a cautely infected with the virus. The present sequence represents a rhesus monkey theta defensin anti-viral peptide, which is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                 Anti-viral, viral infection; theta-defensin; lipid environment; amphipathic alpha-helical structure; virucide; anti-HIV; immunisation; viral growth inhibitor; viral proliferation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New method of using a first anti-viral peptide comprising a Theta-
defensin peptide in an amphipathic Alpha-helical structure in a lipid
environment for reducing the infectivity of a virus.
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                                                                                                                                                                                                                                                                                                     Anti-viral theta defensin peptide RTD-2 SEQ ID NO:28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roller R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stinski M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 10; 65pp; English.
ABP53295 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JAN-2002; 2002WO-US002435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001US-0265270P.
01-AUG-2001; 2001US-0309368P.
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                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maury W, Stapleton J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-674815/72.
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The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as AD03523-54003527. The theta of detailed in the claims or appearing as AD03523-4003527. The theta of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the patient suffering from the antimicrobial activity and low haemolytic activity. The present sequence represents the rhesus monkey wild-type theta defensin RTD-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; SEQ ID NO 2; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-APR-2003; 2003US-00427715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-APR-2002; 2002US-0377071P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Selsted ME, Tran DQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-167945/16.
                                                                                                                                                                                                                                                                                                                    Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                           US2004014669-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ä
                                                                                                                                                                                                                                                                                                                                                                                                                           22-JAN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   object.
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Score 116; DB 8; Pred. No. 8.1e-06;

100.0%;

Query Match Best Local Similarity

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Gaps

. 0

Indels

Length 18;

m

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Gaps

.. 0

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Monkey, Rhesus theta defensin, RTD; antimicrobial peptide; antimicrobial; antinflammatory; antibacterial; virucide; fungicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; disinfectant; fungal infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel theta defensin analog useful for reducing or inhibiting growth survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
 Indels
;
0
                                                                                                                                                   Rhesus theta defensin analogue peptide aRTD-2-OH.
Mismatches
                                                                                                                                                                                                                                                                                                                              /note= "Hydroxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 14; 46pp; English
                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                        ADO35240 standard; peptide; 18 AA
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0
                   18
                               1 GFCRCICTRGFCRCICTR 18
                                                                                                                                                                                                                                                                                                                                                                                                              30-APR-2002; 2002US-0377071P.
                                                                                                                                                                                                                                                                                                                                                                                          30-APR-2003; 2003US-00427715
                    1 GFCRCICTRGFCRCICTR
                                                                                                                                 (first entry)
 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                     3. .16
5. .14
7. .12
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tran DQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-167945/16.
                                                                                                                                                                                                                                                                          Key
Disulfide-bond
Disulfide-bond
Disulfide-bond
Modified-site
                                                                                                                                                                                                                                                                                                                                                 US2004014669-A1
                                                                                                                                                                                                                                              Macaca mulatta
                                                                                                                                 15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Selsted ME,
                                                                                                                                                                                                                                                                                                                                                                     22-JAN-2004
                                                                                                             AD035240;
                                                                                                                                                                                                                                                         Synthetic
 Matches
                                                                                AD035240
                                                                     RESULT
                                                                                                  셤
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The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO3527. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbiscial inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for watering a patient suffering from the peptides are also useful for watering a patient suffering from the peptides are also useful for watering a patient suffering from the peptides are also useful for watering a patient suffering from the peptides are also useful for watering a patient suffering from the peptides are also useful for watering a patient suffering from the peptides are also we full for watering and the present sequence represents a Rhesus theta defensing have

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Sequence 18

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The present invention describes a method (M1) of using a first anti-viral comprising a theta-defensin peptide in an amphipathic alphabetic peptide (I) comprising a theta-defensin peptide in an amphipathic alphabetic beliar structure in a lipid environment for reducing the infectivity of a virus. (I) can have virucles, and and can be used for inhibiting the growth and conce virus growth, infectivity burden, shed, and development of anti-confication of a virus and so can be used for; (a) protecting or treating subject from a viral infection, preventing recurrent viral infection in a subject harbouring a latent virus, controlling virus in subject harbouring a latent virus, controlling virus is spread within a virally-infected subject (V8), reducing virus shed from a V3, reducing percentage of VS in a V8, reducing virus shed from a V3, reducing virus and infection status, or inducing latency in a V8, (b) reducing the infectivity of a virus; and (c) rendering virus.

CC population regardless of viral infection status, or inducing latency in a V8; (b) reducing the infectivity of a virus; and (c) rendering virus.

CC of infectious virus particles in a population of viruses. Wall is useful for reducing the infectivity of a virus in sheep, cattle, horses, swine, cats, fowl and humans e.g. an enveloped virus infecting humans such as human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is continitiested prior to or subsequent to the virus conteacting the subject who is definited by infected with the virus, where the first anti-viral peptide is most preferably administered to a subject who is contonically, latently or acutely infected with the virus acutely infected with the virus anti-viral peptide is most preferably administered to a subject who is contonically, latently or acutely infected with the virus acutely infected with the virus anti-viral peptide is most preferably administered to a subject who is sequence represents a chimeric human/ribected with the virus infected with the virus acutely infec
                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-viral; viral infection; theta-defensin; lipid environment; amphipathic alpha-helical structure; virucide; anti-HIV; immunisation; viral growth inhibitor; viral proliferation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New method of using a first anti-viral peptide comprising a Theta-
defensin peptide in an amphipathic Alpha-helical structure in a lipid
environment for reducing the infectivity of a virus.
                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                        Anti-viral chimeric theta defensin peptide H/RTD-2 SEQ ID NO:32
                                              6
  Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stapleton J, Stinski M, Roller R, Mccray PB,
                                              1; Indels
Score 111; DB 8;
Pred. No. 2.7e-05;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 10; 65pp; English
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                                              .;
0
                                                                                            58
                                                                                                                                        18
                                                                                                                                                                                                                                                       ABP53299 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JAN-2002; 2002WO-US002435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-2001; 2001US-0265270P.
01-AUG-2001; 2001US-0309368P.
  95.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IOWA ) UNIV IOWA RES FOUND
                                                                                                                       GFCRCTCTRGFCRCICTR
                                                                                              1 GFCRCICTRGFCRCICTR
                                                                                                                                                                                                                                                                                                                                                 (first entry)
  Query Match
Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-674815/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macaca mulatta.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                 13-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maury W,
                                                                                                                                                                                                                                                                                                     ABP53299;
                                                                                                                                                                                                              RESULT 5
ABP53299
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us-10-009-317a-32.rag

(first entry)

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Anti-viral, viral infection, theta-defensin, lipid environment, amphipathic alpha-helical structure, virucide, anti-HIV, immunisation, viral growth inhibitor; viral proliferation inhibitor.
                                                                                                                                                                                                                                                                                                                     New method of using a first anti-viral peptide comprising a Theta-defensin peptide in an amphipathic Alpha-helical structure in a lipid environment for reducing the infectivity of a virus.
                                                              Anti-viral theta defensin peptide RTD-1 SEQ ID NO:30.
                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 10; 65pp; English
 ABP53297 standard; peptide; 18 AA
                                                                                                                                                                                                                         2001US-0265270P.
2001US-0309368P.
                                                                                                                                                                                                    29-JAN-2002; 2002WO-US002435
                                                                                                                                                                                                                                                       (IOWA ) UNIV IOWA RES FOUND.
                                                                                                                                                                                                                                                                            Maury W, Stapleton J,
                                                                                                                                                                                                                                                                                                  WPI; 2002-674815/72
                                                                                                                             Macaca mulatta.
                                                                                                                                                          WO200260468-A2
                                                                                                                                                                                                                        30-JAN-2001;
01-AUG-2001;
                                                                                                                                                                                08-AUG-2002,
                                                                                                                                        Synthetic
 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides theta defensin peptides and analogues which have antimicrobial activity. They can be used in the treatment of bacterial, viral, fungal, protozoan and helminthic infections, in disinfectants and as food preservatives
                                                                         Gaps
                                                                                                                                                                                                                                                        Theta defensin, antimicrobial, cyclic, bacterium, fungus, protozoan, virus, helminth; disinfectant, food preservative, analogue.
viral peptide, which is given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel theta defensin peptide with antimicrobial activity against
                                                                          ..
0
                                                                                                                                                                                                                                                                                                                                "peptide bond cyclises the molecule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 101; DB 4; Length 18; Pred. No. 0.0003; l; Mismatches 2; Indels
                                                     Length 18;
                                         Score 103; DB 5; Length 18 Pred. No. 0.00019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bacteria, yeast, fungi, protozoa and viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouellette AJ;
                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                     peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 4; 110pp; English.
                                                                         ő
                                                                                             18
                                                                                                                   18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Selsted ME, Tang Y, Yuan J,
                                                   88.8%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                              10-MAY-2000; 2000WO-US012842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.3%;
                                                                                                                  1 GICKCICTRGFCRCICGR
                                                                                            1 GFCRCICTRGFCRCICTR
                                                                                                                                                                                                                                    Theta defensin SEQ ID NO: 1,
                                                                                                                                                                                                              (first entry)
                                                 Query Match
Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                      1. .18
/note=
3. .16
5. .14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-031853/04.
                                                                                                                                                                     AAB35030 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                         Disulfide-bond
Disulfide-bond
Disulfide-bond
                               Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                    WO200068265-A1
                                                                                                                                                                                                              27-MAR-2001
                                                                                                                                                                                                                                                                                      Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAY-1999;
                                                                                                                                                                                                                                                                                                                     Cross-links
                                                                                                                                                                                                                                                                                                                                                                                                        16-NOV-2000.
           invention
                                                                                                                                               RESULT 6
AAB35030
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m

Mccray PB,

Roller R,

Stinski M,

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The present invention describes a method (M1) of using a first anti-viral peptide (I) comprising a theta-defensin peptide in an amphipathic alphabatical structure in a lighd environment for reducing the infectivity of a virus. (I) can have virucide and anti-HIV activities, and can be used to reduce virus growth, infectivity burden, shed, and development of anti-HIV activities, and can be used to rival resistance. (I) can be used for inhibiting the growth and so can be used for; (a) protecting or treating subject from a viral infection, preventing recurrent viral infection in a subject harbouring a latent virus, controlling virus shed from a VS, reducing percentage of VS in a population regardless of viral infection status, or inducing latency in a VS; (b) reducing the infectivity of a virus; and (c) rendering virus of virus in sheep, cattle, horses, swine, contaminated tissue or fluid sample safe for use, or reducing the number of infectious virus particles in a population of viruses. (M1) is useful for reducing the infectivity of a virus in sheep, cattle, horses, swine, cats, fowl and humans e.g. an enveloped virus infecting humans such as human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is administered to a partient who is immunosuppressed to a cubject who is much infected with the virus, where the first anti-viral peptide is administered prior to or subsequent to the virus of a subject who is contaminated represents a rheas monkey thete defensin anti-viral peptide, which is given in the exemplification of the present invention
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Pred. No. 0.0003;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GFCRCLCRRGVCRCICTR 18
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Ouery Local Similarity 83.53,
Best Local Similarity 83.53,
Best 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 AA;
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Matches

1 GFCRCICTRGFCRCICTR 18

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RESULT 7 ABP53297

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Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .0
                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin-mediated killing is useful for modelling and screening novel antiblocities. The invention is also useful in gene therapy. The present sequence is rhesus monkey theta defensin, RTD1 peptide. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bacterial infection; human pathogen; holin; defensin; peptide nucleic acid; PNA; penicillin; tetracycline; ampicillin; kanamycin; antibiotic; antibacterial; antibiotic-resistance gene; cyclic.
                                                                                                        Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV; human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; rhesus monkey; theta defensin 1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                   New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually
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87.1%; Score 101; DB 6; Length 18;
Best Local Similarity 83.3%; Pred. No. 0.0003;
Matches 15; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                            Hong TB;
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                      AAE33866 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                            Cole AM,
                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 3C; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                       transmitted diseases, vaginosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADD95202 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GFCRCICTRGFCRCICTR 18
                                                                                                                                                                                                                           18-APR-2002; 2002WO-US012353.
                                                                                                                                                                                                                                                 18-APR-2001; 2001US-0284855P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Macaca mulatta RTD1 peptide
                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cyclic defensin fragment.
                                                                                                                                                                                                                                                                       (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                          Lehrer RI, Waring AJ,
                                                                                                                                                                                                                                                                                                                WPI; 2003-103387/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                              Macaca mulatta.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18
                                                                16-APR-2003
                                           AAE33866;
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This invention describes a novel conjugate for treating prokaryotic confidences a transport mediator for passage through the prokaryotic cell membrane and a compound, directed against a prokaryote and intended for introduction into it. The prokaryote is a bacterium, especially one pathogenic in humans. The transport mediator is preferably confidence or adefension. The introduced compound is a peptide or protein, especially a phage-holin protein, its active fragment or variant or a defension. The introduced compound is a peptide nucleic acid (PNA) that inhibits a gene, especially one implicated in resistance to penicillin, tetracycline, ampicillin or knamayoin. The conjugate has the structure transport mediator-spacer-PNA where the spacer is poly(glysine and/or lysine), preferably containing 2-6 amino acids and the spacer is linked to the transport mediator through a claavable disulfide bridge. The conjugates are administered together with antibiotic, by parenteral, transdermal or subcutaneous routes. The products of the invention have antibacterial activity and are used, especially in combination with antibiotics, for treating prokaryotic, especially in combination with antibiotics, for treating prokaryotic, corresistance gene where the PNA is directed against the antibiotic resistance gene. Where the PNA is directed against containing tered antibiotic sensitive to co-administered antibiotics in 'Old' antibiotics can be used successfully in cases where normally they would be ineffective. This sequence represents a cyclic defension fragment described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New conjugate of transport mediator and active agent, useful for treating prokaryotic infections, especially by neutralizing antibiotic resistance
                                       1. .18 ' \mbox{note=} "Residue 1 and residue 18 bond to form a cyclic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Debus J, Pipkorn R, Waldeck W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADD35357 standard; peptide; 18 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JAN-2003; 2003WO-DE000124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JAN-2002; 2002DE-01001862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GFCRCICTRGFCRCICTR
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Best Local Similarity 83.3
Matches 15; Conservative
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3..16
5..14
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                                                                                                                                             Disulfide-bond
Disulfide-bond
Disulfide-bond
           Key
Misc-difference
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                                                                                                                                                                                                                                                                                                  WO2003059392-A2
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24-DEC-2003

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prostaglandin of the P-series and an antimicrobial peptide. A solution of the invention has hypotensive and ophthalmological activity. The solution is useful for the treatment of increased intracoular pressure, such as caused by glaucoma and for the reduction of ocular hypertension. The prostaglandin and the antimicrobial peptide work synergistically, to provide beneficial reduction in the incidence of irritant and toxic side effects such as hyperaemia, irritation and inflammation of conjunctiva, ocular cell dysplasia, irritial melanocyte hyperplasia, and hyperplasmation, associated with the prior art prostaglandin compositions. The present sequence represents an antimicrobial peptide of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rhesus theta defensin-1; RTD-1; bacteraemia; lipopolysaccharide; LPS; lipteichonic acid; LTB; septic shock; antibacterial; fungicide; virucide; immunomodulator; anticoagulant activity; mincrobial cell-wall biosynthesis; immunomodulation; anticoagulant.
                                           antimicrobial; ophthalmic; prostaglandin; hypotensive; ophthalmological; intraocular pressure; glaucoma; ocular hypertension; hyperaemia; irritation; inflammation; conjunctiva; ocular cell dysplasia; iridial melanocyte hyperplasia; hyperpigmentation.
                                                                                                                                                                                                                                                                                                                                                                                                         Ophthalmic solution useful for the treatment of increased intraocular. pressure comprises a prostaglandin of the F-series and an antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel ophthalmic solution comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 101; DB 8; Length 18;
Pred. No. 0.0003;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhesus theta-defensin-1 (RTD-1) peptide.
          Antimicrobial peptide theta-defensin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Page 11; 11pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ā
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                                                                                                                                                                                                                                      21-MAR-2003; 2003WO-US008935
                                                                                                                                                                                                                                                                     21-MAR-2002; 2002US-0367071P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.18;
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Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                       CAYM-) CAYMAN CHEM CO
                                                                                                                                                                                                                                                                                                                                          Johnson J;
                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-011506/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 AA;
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                                                                                                                                  Unidentified
                                                                                                                                                                                                   02-OCT-2003.
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                                                                                                                                                                                                                                                                                                                                           Maxey KM,
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for preparing a composition for treatment and/or prevention of bacteraemia for binding bacterial products such as lipopolysaccharide (LPS) and/or lipteichonic acid (LTA), or for treatment and/or prevention of septic shock RTD-1, isolated from immune cells of rhesus monkeys, has antibacterial, fungicide, virucide, immunomodulator and anticoagulant activity. RTD-1 inhibits microbial cell-wall blosynthesis and also binds activity. RTD-1 inhibits microbial cell-wall blosynthesis and also binds by viruses. RTD-1 combines four advantageous properties: a direct by viruses. RTD-1 combines four advantageous properties: a direct by viruses. RTD-1 combines four advantageous properties: a direct by viruses microbial action, neutralisation of bacterial products (by binding), immunomodulation (reducing release of proinflammatory cytokines but increasing release of regulatory factors) and anticoagulant action, so provides a better and simpler treatment.
                                                                                                                                                                                                            Use of rhesus theta defensin-1 for treating or preventing bacteremia and septic shock, also for binding bacterial products and as immunomodulator and anticoagulant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monkey, Rhesus theta defensin, RTD-1, antimicrobial peptide, cyclic, antimicrobial, antinflammatory, antibacterial, virucide, fungicide; food, contact lens solution, eye wash solution; inflammatory response; microbicidal inhibition, microbistatic growth inhibition; disinfectant; food preservative; bacterial infection, viral infection; disinfectant; fungal infection; haemolytic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps

    18 /note= "The peptide is cyclised by a covalent link
between these two residues"

                                                                                                                                                                                                                                                                                                                          This invention describes the novel use of rhesus theta defensin-1
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                                                                                                                                           Gerdes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                           Brunner N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                           Labischinski H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhesus theta defensin peptide, RTD-1.
                                                                                                                                                                                                                                                                                        Example 1; SEQ ID NO 1; 28pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADO35229 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18
                                  30-MAY-2003; 2003WO-EP005694.
                                                                     13-JUN-2002; 2002DE-01026216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 83.3%;
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FARB ) BAYER HEALTHCARE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                           Ladel C, Newton B,
                                                                                                                                                                               WPI; 2004-071500/07
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Disulfide-bond
Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18 AA;
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Modified-site
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30-APR-2003; 2003US-00427715.
                                                                                   30-APR-2002; 2002US-0377071P.
                                                                                                           (REGC ) UNIV CALIFORNIA.
            US2004014669-A1.
                                                                                                                                      Selsted ME,
                                    22-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO3527. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensing have high antimicrobial activity and low haemolytic activity. The present sequence represents the rhesus monkey wild-type theta defensin RTD-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monkey; Rhesus theta defensin; RTD; antimicrobial peptide; antimicrobial; antilnflammatory; antibacterial; virucide; fungicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; disinfectant; fungal infection; haemolytic activity.
                                                                                                                                                 Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 101; DB 8; Length 18;
Pred. No. 0.0003;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhesus theta defensin analogue peptide aRTD-1-OH.
                                                                                                                                                                                                                Example 1; SEQ ID NO 1; 46pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.1%;
                         30-APR-2003; 2003US-00427715.
                                                 30-APR-2002; 2002US-0377071P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GFCRCICTRGFCRCICTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                        (REGC ) UNIV CALIFORNIA.
                                                                                                   Tran DQ;
                                                                                                                           WPI; 2004-167945/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Macaca mulatta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-2004
 22-JAN-2004.
                                                                                                   Selsted ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AD035238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
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The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO35257. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of an acroorganism in an environment such as food or growth or survival of a microorganism in an environment such as food or cod product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbistatic inhibition of survival of microorganism as well as the reapeutic agents, disinfectants, food preservatives, or medicaments. The appendes are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensing have betterial, viral, fungal or other infection. The theta defensing have high antimicrobial activity and low haemolytic activity. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monkey; Rhesus theta defensin; RTD; antimicrobial peptide; antimicrobial; antinflammatory; antibacterial; virucide; fungicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbicidalstatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; disinfectant; fungal infection; haemolytic activity.
                                                           Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence represents a Rhesus theta defensin analogue peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.1%; Score 101; DB 8; Length 18; 83.3%; Pred. No. 0.0003; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhesus theta defensin analogue peptide aRTD-1-NH.
                                                                                                                                                                                                                                                            Example 2; SEQ ID NO 12; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
3. .16
5. .14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADO35239 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GFCRCICTRGFCRCICTR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 83.3
Matches 15; Conservative
WPI; 2004-167945/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Macaca mulatta.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-2004
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                                                                                                                                                                                             object.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
ADO35239
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1. .18 /note= "The peptide is cyclised by a covalent link

Location/Qualifiers

Key Modified-site

between these two residues"

Disulfide-bond

30-APR-2003; 2003US-00427715. 30-APR-2002; 2002US-0377071P.

US2004014669-A1 Disulfide-bond Disulfide-bond

22-JAN-2004.

(REGC) UNIV CALIFORNIA. Selsted ME, Tran DQ, WPI; 2004-167945/16.

7. .12

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Monkey; Rhesus theta defensin; RTD; antimicrobial peptide; antimicrobial; antinflammatory; antibacterial; virucide; fungicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbicatatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; disinfectant; fungal infection; haemolytic activity; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhesus theta defensin analogue peptide RTD-1-26.
                                                                                                                                                                                                                                                                                                                                                                                                                       ADO35250 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-2004 (first entry)
Disulfide-bond
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macaca mulatta.
Synthetic.
                                             22-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                      AD035250;
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
ADO35250
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The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as AD035239-AD035257. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism and is useful for reducing prowth or survival of the microorganism and is useful for reducing or inhibiting rowth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for dicroorganism as well as microbistatic inhibition of survival of microorganism as well as the proposition inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from a pactual, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents a Rhesus thera defensin analogue peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 101; DB 8; Length 18;
Pred. No. 0.0003;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 13; 46pp; English
/note= "Amidated"
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                                                                                                                                                                                                              30-APR-2003; 2003US-00427715.
                                                                                                                                                                                                                                                                                       30-APR-2002; 2002US-0377071P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GFCRCLCRRGVCRCICTR
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Best Local Similarity 83.3%
                                                                                                                                                                                                                                                                                                                                                        (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                 Selsted ME, Tran DQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-167945/16.
                                                                    US2004014669-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 AA;
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OF

Novel theta defensin analog useful for reducing or inhibiting growth survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate

Claim 1; SEQ ID NO 24; 46pp; English.

object.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        defension the claims or appearing as ADOS239-ADOS2557. The thete defension analogue is useful for reducing or inhibiting growth or survival of a microorganism and is useful for reducing or inhibiting growth or survival of the microorganism and is useful for reducing or inhibiting prowth or survival of the microorganism in an environment such as food or food product, as colution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a manmal. The microbicidal inhibition of survival of microorganism as well as microbicidal inhibition of survival of microorganism as well as microbicidismition of growth. Thus the peptides are useful as the peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The thete defensins have high antimicrobial activity and low haemolytic activity. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monkey, Rhesus theta defensin, RTD-1, antimicrobial peptide, antimicrobial, antinflammatory, antibacterial; virucide, fungicide, food, contact lens solution; eye wash solution; inflammatory response, microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; disinfectant; fungal infection; haemolytic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a theta defensin analogue defined by formulae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence represents a Rhesus theta defensin analogue peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.1%; Score 101; DB 8; Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monkey RTD-1 (rhesus theta defensin 1) 2X protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 0.0003;
); Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AD035263 standard; protein; 38 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GFCRCTRGFCICTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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AD035255 standard, peptide; 18 AA.
  Macaca mulatta
                     Cleavage-site
           Cleavage-site
                                                                                                                                                                       15-JUL-2004
                                                        Selsted ME,
                                     22-JAN-2004
    Synthetic
                                                                                                                                                                  AD035255;
                Peptide
                                                                                                                                                         RESULT 17
                                                                                                                                                           AD035255
à
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WPI; 2004-167945/16. US2004014669-A1. Sequence 18 AA; Disulfide-bond Disulfide-bond Disulfide-bond Macaca mulatta. Key Modified-site 22-JAN-2004 Selsted ME, Synthetic Query Match à The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as AD035239-AD03527. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for the activity. The present suffering protein containing 2 copies of the rhead defensing have ö Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate Gaps .. 0 Score 101; DB 8; Length 38; Pred. No. 0.00052; 1; Mismatches 2; Indels Location/Qualifiers
1..2
/note= "CNBr cleavage site"
2..19
/note= "RTD-1" 20. .21 /note= "CNBr cleavage site" 21. .38 /note= "RTD-1" Example 4; Fig 17a; 46pp; English. 78 30-APR-2002; 2002US-0377071P. 30-APR-2003; 2003US-00427715. 87.18; 2 GFCRCLCRRGVCRCICTR 1 GFCRCICTRGFCRCICTR Conservative (REGC) UNIV CALIFORNIA Tran DQ; WPI; 2004-167945/16. N-PSDB; ADO35262. US2004014669-A1 Sequence 38 AA;

Query Match Best Local Similarity Matches 15; Conserv

(first entry)

Monkey; Rhesus theta defensin; RTD; antimicrobial peptide; antimicrobial; antilnflammatory; antibacterial; virucide; fungicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; disinfectant; fungal infection; haemolytic activity; cyclic. Rhesus theta defensin analogue peptide RTD-4.

 .18 /note= "The peptide is cyclised by a covalent link between these two residues" Location/Qualifiers

3. .16 5. .14 7. .12

30-APR-2003; 2003US-00427715.

30-APR-2002; 2002US-0377071P.

(REGC) UNIV CALIFORNIA

Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate

Claim 1; SEQ ID NO 29; 46pp; English.

The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO35257. The theta defeated in the claims or appearing as ADO35239-ADO35257. The theta defeating an anticopy of the state of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting control of the microorganism in an environment such as food or growth or survival of a microorganism in an environment such as food or control, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present constructive in the present in the present and in an analogue peptide.

Gaps . 0 Length 18; 86.2%; Score 100; DB 8; Length 18 93.8%; Pred. No. 0.00038; tive 0; Mismatches 1; Indels 93.8%; Pre Best Local Similarity 93.8
Matches 15; Conservative

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1 GFCRCICTRGFCRCIC 16

AAE33805 standard; peptide; 18 AA. RESULT 18
AAE33805
ID AAE33
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form

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AAE33805

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The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin-mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is human retrocyclin peptide analogue
                                                                               Retrocyclin, infection, sexually transmitted disease, gene therapy, HIV, human immunodeficiency virus, bacterial vaginosis, ophthalmic infection, antibiotic modelling, antimicrobial; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually transmitted diseases, vaginosis.
                                                                                                                                                                                       /note= "Linked to amino acid at position 18 to cyclic structure"
                                                                                                                                                                                                                                                                               /note= "Linked to amino acid at position 1 cyclic structure"
                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IllY retrocyclin peptide analogue
                                                       retrocyclin peptide analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cole AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 9; Page 24; 72pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.2%;
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                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waring AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-103387/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                        Disulfide-bond 3
Disulfide-bond 5
Disulfide-bond 7
Misc-difference 1
                                                                                                                                                                  Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18 AA;
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                            16-APR-2003
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Matches
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Hong TB;

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Gaps

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Score 93; DB 6; Length 18; Pred. No. 0.0021; 1; Mismatches 3; Indels

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18

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is human retrocyclin peptide analogue
          Retrocyclin, infection, sexually transmitted disease, gene therapy; HIV; human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   retrocyclin; cyclic; primate; retroviral infection; circular minidefensin; antibacterial; virucide; vaccine; immunotherapy; microbial; viral; human.
                                                                                                                       ಗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                      form
                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually
                                                                                                                                                                                               /note= "Linked to amino acid at position 1 to form cyclic structure"
                                                                                                                       to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                    /note= "Linked to amino acid at position 18
cyclic structure"
3. .16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; DB 6; Leus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                Hong TB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 93;
Pred. No.
                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RC-104.
                                                                                                                                                                                                                                                                                                                                                                                Cole AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transmitted diseases, vaginosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 9; Page 24; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18
                                                                                                                                                                                                                                                                                                  18-APR-2002; 2002WO-US012353.
                                                                                                                                                                                                                                                                                                                            18-APR-2001; 2001US-0284855P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.2%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GFCRCICTRGFCRCICTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADN08180 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human retrocyclin peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-2004. (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 77.8
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                   (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                Waring AJ,
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-103387/09.
                                                                                                                                               Disulfide-bond 3
Disulfide-bond 5
Disulfide-bond 7
Misc-difference 1
                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 AA;
                                                                                                                                                                                                                                             WO200285401-A1
                                                                  Unidentified
                                                                                                                                                                                                                                                                     31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                Lehrer RI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADN08180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADN08180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
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UNIV CALIFORNIA.

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06-MAY-2003; 2003WO-US014106
                                                                       06-MAY-2002; 2002US-00141645
WO2004033479-A2.
                        22-APR-2004
                                                                                              (REGC)
(LEHR/)
                                                                                                                        (WARI/)
 ò
                                                                                                                                                                                                                                                                                                                        The invention relates to a novel isolated retrocyclin peptide. The invention further provides: a cyclic polypeptide; an isolated nucleic convention further provides: a cyclic polypeptide; an isolated nucleic infection in a cell by administering an effective dose of a circular minidefension or retrocyclin, a method for killing microbial corganisms; a method for administering restrocyclin to the microbial organisms; a method for administering restrocyclin as a microbial organisms; a method for administering restrocyclin as a infection; and a method for administering retrocyclin as a prophlactic agent to prevent a microbial or viral infection; and a method for administering retrocyclin as a prophlactic agent to prevent a microbial or viral infection in a patient at risk of developing such infection. The retrocyclin peptide can be used to treat a viral infection such as HIV-1. The retrocyclin peptide can be used as a vaccine or an beused in immunotherapy. The peptide and polypeptides are useful as therapeutic and prophlactic agents for treating and preventing microbial and viral infections. This sequence represents a retrocyclin
                                                                                                                                                                                                                                                     New isolated retrocyclin peptides and cyclic polypeptides, useful as therapeutic and prophylactic agents for treating and preventing microbial and viral infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        retrocyclin, cyclic; primate; retroviral infection; circular minidefensin; antibacterial; virucide; vaccine; immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80.2%; Score 93; DB 8; Length 18; 77.8%; Pred. No. 0.0021; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                      Cole AM, Hong TB;
                                                                                                                                                                                                                                                                                                      Claim 9; SEQ ID NO 5; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human retrocyclin peptide, RC-105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADN08181 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GFCRCICTRGFCRCICTR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GYCRCICGRGICRCICGR 18
                                                                                  06-MAY-2003; 2003WO-US014106.
                                                                                                         06-MAY-2002; 2002US-00141645.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 77.8
nes 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  microbial; viral; human.
                                                                                                                              (REGC ) UNIV CALIFORNIA.
(LEHR/) LEHRER R I.
                                                                                                                                                                                                      cehrer RI, Waring AJ,
                                                                                                                                           LEHRER R I.
WARING A J.
COLE A M.
HONG T B.
                                                                                                                                                                                                                              WPI; 2004-340883/31.
                                   WO2004033479-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18 AA;
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
Synthetic.
                                                          22-APR-2004
           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                (HONG/)
                                                                                                                                                       (WARI/)
                                                                                                                                                                   (COLE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
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g
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The introduction features to a novel isolated retrocycling peptide. The interpretation is each a novel isolated retrocycling an isolated mucleic acid encoding a primate retrocyclin; a method for preventing retroviral infection in a cell by administering an effective dose of a circular minidefensin or retrocyclin to each cell; a method for killing microbial organisms by administering an effective dose of retrocyclin to the organisms by administering an effective dose of retrocyclin to the microbial organism; a method for administering retrocyclin as a therapeutic agent to a patient with an established microbial or viral infection, and a method for administering retrocyclin as a prophylactic agent to prevent a microbial or viral infection in a patient at risk of agent to prevent and microbial or viral infection in peptide has antibacterial and viral such as HIV-1. The retrocyclin peptide can be used to treat a viral infection such as HIV-1. The retrocyclin peptide can be used as a vaccine and can be used in immunotherapy. The peptide and polypeptides are useful as therapeutic and prophylactic agents for treating and preventing microbial and viral infections. This sequence represents a retrocyclin
                                                                                                                                                                                                                                                                                                                                             New isolated retrocyclin peptides and cyclic polypeptides, useful as therapeutic and prophylactic agents for treating and preventing microbial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Theta defensin; antimicrobial; cyclic; bacterium; fungus; protozoan; virus; helminth; disinfectant; food preservative; analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel isolated retrocyclin peptide. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80.2%; Score 93; DB 8; Length 18; 77.8%; Pred. No. 0.0021; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhesus macaque theta defensin peptide SEQ ID NO: 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; SEQ ID NO 6; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB35037 standard; peptide; 18 AA.
                                                                                                                                                                                                Cole AM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GFCRCICTRGFCRCICTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GICRCICGRGYCRCICGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 77.89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide of the invention.
                                                                                                                                                                                                Lehrer RI, Waring AJ,
LEHRER R I.
WARING A J.
COLE A M.
HONG T B.
                                                                                                                                                                                                                                                                        WPI; 2004-340883/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhesus macaque.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200068265-A1
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                                                                                (COLE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 22
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The present invention describes a method (M1) of using a first anti-viral peptide (I) comprising a theta-defensin peptide in an amphipathic alpha-helical structure in a lipid environment for reducing the infectivity of a virus. (I) can have virucide and anti-HIV activities, and can be used to reduce virus growth, infectivity burden, shed, and development of anti
                                                                                                                                                                                                                 The present invention provides theta defensin peptides and analogues which have antimicrobial activity. They can be used in the treatment of bacterial, viral, fungal, protozoan and helminthic infections, in disinfectants and as food preservatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-viral, viral infection, theta-defensin, lipid environment, amphipathic alpha-helical structure, virucide, anti-HIV, immunisation, viral growth inhibitor, viral proliferation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New method of using a first anti-viral peptide comprising a Theta-defensin peptide in an amphipathic Alpha-helical structure in a lipid environment for reducing the infectivity of a virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic anti-viral human theta defensin peptide HTD-1 SEQ ID NO:27
                                                                                                                                        Novel theta defensin peptide with antimicrobial activity against
bacteria, yeast, fungi, protozoa and viruses.
                                                                                                                                                                                                                                                                                                                             Query Match
78.4%; Score 91; DB 4; Length 18;
Best Local Similarity 81.2%; Pred. No. 0.0033;
Matches 13; Conservative 1; Mismatches 2; Indels
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                                                                            Ouellette AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stinski M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 9; 65pp; English.
                                                                                                                                                                                   Example 1; Fig 2; 110pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP53294 standard; peptide; 18
                                                                            Yuan J,
                99US-00309487
                                                                                                                                                                                                                                                                                                                                                                                             GFCRCICTRGFCRCIC 16
                                                                                                                                                                                                                                                                                                                                                                                                             GFCRCLCRRGVCRCIC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JAN-2002; 2002WO-US002435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001US-0265270P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IOWA ) UNIV IOWA RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                            (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stapleton J,
                                                                                                                                      Novel theta defensin
                                                                          Tang Y,
                                                                                                          WPI; 2001-031853/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-674815/72.
                                                                                                                                                                                                                                                                                                 Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200260468-A2
                10-MAY-1999;
                                                                          Selsted ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maury W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2:
ABP53294
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Mccray PB,

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containing subject from be used for inhibiting the growth and proliferation of a virus and so can be used for; (a) protecting or treating subject from a viral infection, preventing recurrent virus infection in a subject harbouring a latent virus, controlling virus spread within a virally-infected subject (VS), reducing virus burden in a VS, reducing virus seed within a virally-infected subject (VS), reducing virus burden in a VS, reducing virus sheed from a VS, reducing percencage of VS; in a population regardless of viral infection status, or inducing latency in a VS; (b) reducing the infectivity of a virus; and (c) rendering virus-contaminated tissue or fluid sample safe for use, or reducing the number of infectious virus particles in a population of viruses. (M1) is useful contaminated the infectivity of a virus in sheep, cattle, horses, swine, cats, fowl and humans e.g. an enveloped virus infecting humans such as human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is not infected with the virus, where the first anti-viral peptide is administered prior to or subsequent to the virus contacting the subject. The anti-viral peptide is most preferably administered to a subject who is contaminally, latently or subsequent to the virus contacting the subject. The anti-viral peptide is most preferably administered to a subject who is such an in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Retrocyclin, infection, sexually transmitted disease, gene therapy, HIV; human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; human; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to form a
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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cyclic structure"
                                                                                                                                                                                                                                                                                                                                                                                                                Score 90; DB 5; Length 18; Pred. No. 0.0043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE33801 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GFCRCICTRGFCRCICTR 18
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                                                                                                                                                                                                                                                                                                                                                                                                              77.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human retrocyclin peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (REGC ) UNIV CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-103387/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Misc-difference
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Disulfide-bond
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lehrer RI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE33801;
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Gaps

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Length 18;

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transmitted diseases, vaginosis
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(COLE/)
(HONG/)
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(LEHR/)
                                                                                                                                                                                                                                             RESULT 26
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                                                                                                                                                                                                            임
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                                                                   The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin-mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is human retrocyclin peptide
                                                                                                                                                                                                                                                                                                                                                                            Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV; human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Linked to amino acid at position 18 to form a cyclic structure"
3. .16
5. .14
7. .12
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually
 New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually transmitted diseases, vaginosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Linked to amino acid at position 1 to form cyclic structure"
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                                                                                                                                                                                Score 90; DB 6; Length 18;
Pred. No. 0.0043;
); Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hong TB;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. .18
/note= "D-form residues"
                                                                                                                                                                                                                                                                                                                                                            Enantio-retrocyclin peptide analogue.
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                                                   Claim 9; Page 24; 72pp; English
                                                                                                                                                                                                                                                                                                  AAE33863 standard; peptide; 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-APR-2001; 2001US-0284855P
                                                                                                                                                                                  Query Match
Best Local Similarity 77.8%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                        (first entry)
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Disulfide-bond 5
Disulfide-bond 7
Misc-difference 1
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Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                 Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
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                                                The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin-mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is human retrocyclin peptide analogue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   retrocyclin, cyclic, primate, retroviral infection; circular minidefensin; antibacterial; virucide; vaccine; immunotherapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
77.6%; Score 90; DB 6;
Best Local Similarity 77.8%; Pred. No. 0.0043;
Matches 14; Conservative 0; Mismatches 4
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Disclosure; Page 24; 72pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNIV CALIFORNIA.
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and viral infections.
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WARING A J.
COLE A M.
HONG T B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-340883/31.
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                                                                                                                                                                                                                                                                                                                                                             Sequence 18
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infection, and a method for administering retrocyclin as a prophylactic agent to prevent a microbial or viral infection in a patient at risk of developing such infection. The retrocyclin peptide has antibacterial and virucide activities. The retrocyclin peptide can be used to treat a viral infection such as HIV-1. The retrocyclin peptide can be used as a vaccine and can be used in immunotherapy. The peptide and polypeptides are useful as therapeutic and prophylactic agents for treating and preventing microbial and viral infections. This sequence represents a retrocyclin peptide of the invention.
                                                                                                                                                                                                                                                                                                                    Sequence 18 AA;
            88888888888888888
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Score 90; DB 8; Length 18;
Pred. No. 0.0043;
0; Mismatches 4; Indels
                       0; Mismatches
                                             18
                                                                   18
77.6%;
                                                           GICRCICGRGICRCICGR
                                             1 GFCRCICTRGFCRCICTR
                       14; Conservative
              Best Local Similarity
  Query Match
                      Matches
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Gaps

RESULT 27 AD035249

ADO35249 standard; peptide; 18 AA.

ADO35249;

(first entry) 15-JUL-2004 Rhesus theta defensin analogue peptide RTD-1-25.

Monkey, Rhesus theta defensin, RTD, antimicrobial peptide, antimicrobial, antiinflammatory, antibacterial, virucide, fungicide, food, contact lens solution, eye wash solution, inflammatory response, microbicidal inhibition, microbisterio growth inhibition, disinfectant, food preservative, bacterial infection, viral infection, disinfectant fungal infection, haemolytic activity, cyclic.

Macaca mulatta.

Synthetic

1 .18 /note= "The peptide is cyclised by a covalent link between these two residues" Location/Qualifiers Modified-site

Disulfide-bond Disulfide-bond Disulfide-bond

US2004014669-A1

22-JAN-2004.

30-APR-2003; 2003US-00427715

30-APR-2002; 2002US-0377071P. (REGC) UNIV CALIFORNIA.

Selsted ME, Tran DQ;

WPI; 2004-167945/16.

Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate object.

Claim 1; SEQ ID NO 23; 46pp; English.

The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as AD035239-AD035257. The theta defensin analogue is useful for reducing or inhibiting growth or survival

ö of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of survival of microorganism as well as marcobisatatic inhibition of growth. Thus the peptides are useful as the repetides are also useful for treating a patient suffering from Dacterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents a Rhesus theta defensin analogue peptide. Gaps 76.7%; Score 89; DB 8; Length 18; 77.8%; Pred. No. 0.0054; ive 0; Mismatches 4; Indels 18 1,8 1 GFCRCICTRGFCRCICTR GFCRCRCRRGVCLCICTR Local Similarity 77.8 Sequence 18 AA; Query Match Matches 888888888888888888888888 셤 à

ABP53298 standard; peptide; 18 AA

ABP53298;

(first entry) 13-NOV-2002

Anti-viral chimeric theta defensin peptide H/RTD-3 SEQ ID NO:31

Anti-viral, viral infection, theta-defensin, lipid environment, amphipathic alpha-helical structure, virucide, anti-HIV, immunisation, viral growth inhibitor, viral proliferation inhibitor.

Homo sapiens

Macaca mulatta. Synthetic.

WO200260468-A2. 08-AUG-2002. 29-JAN-2002; 2002WO-US002435.

30-JAN-2001; 2001US-0265270P. 01-AUG-2001; 2001US-0309368P.

(IOWA) UNIV IOWA RES FOUND.

Roller R, Stinski M, Maury W, Stapleton J, WPI; 2002-674815/72.

э Э Tack

Mccray PB,

New method of using a first anti-viral peptide comprising a Theta-defensin peptide in an amphipathic Alpha-helical structure in a lipid environment for reducing the infectivity of a virus.

Disclosure; Page 10; 65pp; English.

The present invention describes a method (MI) of using a first anti-viral peptide (I) comprising a theta-defensin peptide in an amphipathic alphahilaal structure in a lipid environment for reducing the infectivity of a virus. (I) can have virucide and anti-HIV activities, and can be used to reduce virus growth, infectivity burden, shed, and development of anti-viral resistance. (I) can be used for inhibiting the growth and proliferation of a virus and so can be used for; (a) protecting or treating subject from a viral infection, preventing recurrent viral infection in a subject harbouring a latent virus, controlling virus

us-10-009-317a-32.rag

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spread within a virally-infected subject (VS), reducing viral burden in a VS, reducing virus shed from a VS, reducing percentage of VS in a US, reducing virus shed from a VS, reducing percentage of VS in a containation regardless of viral infection status, or inducing latency in a VS, (b) reducing the infectivity of a virus; and (c) rendering virus-containated tissue or fluid sample safe for use, or reducing the number of infectious virus particles in a population of viruses. (MI) is useful for reducing the infectivity of a virus in sheep, cattle, horses, swine, cats, fowl and humans e.g. an enveloped virus infecting humans such as human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is administered to a patient who is immunosuppressed or to a subject who is not infected with the virus, where the first anti-viral peptide is administered prior to or subsequent to the virus contacting the subject. The anti-viral peptide is most preferably administered to a subject who is contacting represents a chimeric human/rhesus monkey theta defensin anti-viral peptide, which is given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pore forming agents and/or for the storage and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transplant, antimicrobial peptide; pore forming agent, cardioplegia; cell surface receptor binding compound; kidney transplant; cardioplegia; organ transplant; transplant rejection; defensin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes new transplant compositions comprising antimicrobial polypeptides or pore forming agents and/or cell surface receptor binding compounds. The media is capable of extending the preservation period past 72 hours and can provide organs with increased functionality upon transplant, animals receiving kidneys stored in the media of the present invention for either three or four days had serum
                                                                                                                                                                                                                                                                                                                                                                                                          Score 88; DB 5; Length 18;
Pred. No. 0.0069;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transplant media associated defensin peptide #1\dot{	extstyle}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Media comprising antimicrobial polypeptides or cell surface receptor binding compounds useful preservation of organs prior to transplant.
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17-NOV-2000; 2000US-0249602P.
15-MAY-2001; 2001US-0290932P.
                                                                                                                                                                                                                                                                                                                                                                                                              75.9%;
72.2%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                          Sequence 18 AA;
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Gaps ..

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creatinine levels of less than half of those observed in control animals receiving kidneys stored in UW solution (defined in the specification) alone. Lower serum creatinine levels are indicative of healthier kidneys and a more preferable prognosis for the transplant patient. The media of the invention are useful for decreasing the incidence and/or severity of delayed graft function in patients receiving transplanted kidneys stored and/or treated in the media. The media may also be used in procedures such as cardioplegia. It is contemplated that transplant of healthier organs leads to a decrease in chronic rejection. This sequence represents an antimicrobial defensin peptide studied in the development of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV; human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; cyclic.
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3. .16
5. .14
7. .12
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cyclic structure"
                                                                                                                                                                                                                           Query Match 75.0%; Score 87; DB 5; Length 18; Best Local Similarity 86.7%; Pred. No. 0.0088; Matches 13; Conservative 1; Mismatches 1; Indels
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1. .18
/note= "D-form residues"
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Disulfide-bond
Disulfide-bond
Misc-difference
                                                                                                                                                                    transplant media
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                                                                                                                                                                                                  Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
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Synthetic.
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(LEHR/)
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                                                                                                                                                                                                                                                                                                                  RESULT 3:
ADN08177
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The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin mediated killing is useful for modalling and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is human retrocyclin peptide analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Retrocyclin, infection, sexually transmitted disease, gene therapy, HIV, human immunodeficiency virus, bacterial vaginosis, ophthalmic infection, antibiotic modelling, antimicrobial; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Linked to amino acid at position 18 to form a cyclic structure"
3. .16
5. .14
7. .12
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually transmitted diseases.
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                                                                                                                                                                                                                                 Score 87; DB 6; Length 18;
Pred. No. 0.0088;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hong TB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R9K retrocyclin peptide analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cole AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cyclic structure"
                                                                                                                                                                                                                                                                                                                  18
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE33802 standard; peptide; 18
                                                                                                                                                                                                                               75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-APR-2001; 2001US-0284855P.
                                                                                                                                                                                                                                                                                                                                                         1 GickcicekGickcicek
                                                                                                                                                                                                                                                                                                                  1 GFCRCICTRGFCRCICTR
                                                                                                                                                                                                                      Ouery Match 72.2' Best Local Similarity 72.2'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-103387/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Misc-difference
                                                                                                                                                                                         Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200285401-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE33802;
                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 31
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The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The

Claim 9; Page 24; 72pp; English.

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The invention relates to a novel isolated retrocyclin peptide. The invention further provides: a cyclic polypeptide; an isolated nucleic acid ancoding a primate retrocyclin; a method for preventing retroviral infection in a cell by administering an effective dose of a circular mindefensin or retrocyclin to the cell; a method for xilling microbial organisms by administering an effective dose of retrocyclin to the microbial organisms; a method for administering restrocyclin as a therapeutic agent to a patient with an established microbial or viral infection; and method for administering restrocyclin as a prophytactic agent to prevent a microbial or viral infection in a patient at risk of developing such infection. The retrocyclin peptide has antibacterial and infection such as HIV-1. The retrocyclin peptide can be used as a vaccine and can be used in immunotherapy. The peptide and polypeptides are useful and viral infections. This sequence represents a retrocyclin peptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated retrocyclin peptides and cyclic polypeptides, useful as therapeutic and prophylactic agents for treating and preventing microbial and viral infections.
retrocyclin-mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is human retrocyclin peptide analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                retrocyclin; cyclic; primate; retroviral infection; circular minidefensin; antibacterial; virucide; vaccine; immunotherapy; microbial; viral; human.
                                                                                                                                           Gaps
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0
                                                                                         Score 87; DB 6; Length 15;
Pred. No. 0.0088;
                                                                                                                                         1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 9; SEQ ID NO 2; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                      Human retrocyclin peptide, RC-101.
                                                                                                                                                                                                                                                                                                 ADNO8177 standard; peptide; 18 AA
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                                                                                                    ch 75.0%;
1 Similarity 72.2%;
13; Conservative
                                                                                                                                                                            1 GFCRCICTRGFCRCICTR
                                                                                                                                                                                                       1 GICRCICGRGICRCICGR
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LEHRER R I.
WARING A J.
COLE A M.
HONG T B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waring AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-340883/31.
                                                                                                      Query Match
Best Local Similarity
Matches 13; Conserv
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                                                                       Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                     15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-APR-2004.
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us-10-009-317a-32.rag

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The present invention describes a method (M1) of using a first anti-viral peptide (I) comprising a thera-defensin peptide in an amphipathic alphace peptide (I) comprising a thera-defensin peptide in an amphipathic alphact peptide is structure in a lipid environment for reducing the infectivity of a virus. (I) can have virucide and anti-HIV activities, and can be used for including the growth and conce virus and so can be used for inhibiting the growth and concernation of a virus and so can be used for; (a) protecting or treating subject from a viral infection, preventing recurrent viral infection in a subject harbouring a latent virus, controlling virus in subject harbouring a latent virus, controlling virus shed from a VS, reducing virus shed from a VS, reducing virus latency in a VS, reducing virus shed from a VS, reducing virus infections in infections virus and (c) rendering latency in a VS, (b) reducing the infectivity of a virus; and (c) rendering virus.

CC of infectious virus particles in a population of viruses. (M1) is useful for reducing the infectivity of a virus in sheep, cattle, horses, swine, cortain manunodeficiency virus (HIV). Preferably, the anti-viral peptide is containistered prior to a subsequent to the virus contacting the subject. The anti-viral peptide is most preferably administered to a patient who is immunosuppressed or to a subject who is contacting the virus. The present contacting peptide is containistered to a patient whose the first anti-viral peptide is contacting in the exemplification of the present invention in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                             New method of using a first anti-viral peptide comprising a Theta-defensin peptide in an amphipathic Alpha-helical structure in a lipid environment for reducing the infectivity of a virus.
amphipathic alpha-helical structure, virucide, anti-HIV, immunisation; viral growth inhibitor, viral proliferation inhibitor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.1%; Score 86; DB 5; Length 18; 66.7%; Pred. No. 0.011; ive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                             Mccray PB,
                                                                                                                                                                                                                                                                                             Roller R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhesus theta defensin peptide, RTD-3.
                                                                                                                                                                                                                                                                                               Stinski M,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Page 10; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ä.
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                                                                                                                                                                                                         30-JAN-2001; 2001US-0265270P.
01-AUG-2001; 2001US-0309368P.
                                                                                                                                                                          29-JAN-2002; 2002WO-US002435.
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nes 12; Conservative
                                                                                                                                                                                                                                                                                               Stapleton J,
                                                                                                                                                                                                                                                                                                                                WPI; 2002-674815/72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 18 AA;
                                                      Macaca mulatta.
Synthetic.
                                                                                                         WO200260468-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-2004
                                                                                                                                            08-AUG-2002
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                                                                                                                                                                                                                                                                                               Maury W,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides theta defensin peptides and analogues which have antimicrobial activity. They can be used in the treatment of bacterial, viral, fungal, protozoan and helminthic infections, in disinfectants and as food preservatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                    Theta defensin; antimicrobial; cyclic; bacterium; fungus; protozoan; virus; helminth; disinfectant; food preservative; analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel theta defensin peptide with antimicrobial activity against bacteria, yeast, fungi, protozoa and viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-viral; viral infection; theta-defensin; lipid environment;
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                                                    Score 87; DB 8; Length 18;
Pred. No. 0.0088;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.1%; Score 86; DB 4; Length 18; 66.7%; Pred. No. 0.011; 1ive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-viral theta defensin peptide RTD-3 SEQ ID NO:29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouellette AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ä
                                                                                                                                                                                                                                                AAB35047 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP53296 standard; peptide; 18
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                                                                                                                             18
                                                                                                                                             1 GICRCICGKGICRCICGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang Y, Yuan J,
                                                      75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-MAY-2000; 2000WO-US012842.
                                                                                                                                                                                                                                                                                                                                                  Theta defensin SEQ ID NO: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .0-MAY-1999; 99US-00309487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GVCRCLCRRGVCRCLCRR
                                                                                                                             1 GFCRCICTRGFCRCICTR
                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                        Local Similarity 72.2
nes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (REGC ) UNIV CALIFORNIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18 AA;
                         Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40200068265-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Selsted ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
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                                                                                                                                                                                                                                                                                                                   27-MAR-2001
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                                                        Query Match
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Matches
                                                                                          Matches
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Gaps

(first entry)

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object.
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ADO35242 standard; peptide; 18 AA.

RESULT 36 AD035242

AD035242

GVCRCLCRRGVCRCLCRR

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Rhesus theta defensin analogue peptide aRTD-3-NH
The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as AD03523-30-AD03527. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism and is useful for reducing or inhibiting rowth or survival of the microorganism and is useful for reducing or inhibiting trowth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbistatic inhibition of survival of microorganism as well as the appendes are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful suffering a patient suffering from the peptides are also useful suffering a patient suffering from the peptides are also useful suffering a patient suffering from the peptides are also useful suffering a patient suffering from the peptides are also useful suffering a patient suffering from the peptides are also useful suffering a patient suffering from the peptides are also useful suffering from the peptides ar
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                     Monkey, Rhesus theta defensin, RTD-3; antimicrobial peptide, cyclic, antimicrobial, antinflammatory, antibacterial; virucide, fungicide, food; contact lens solution; eye wash solution; inflammatory response, microbicidal inhibition, microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; disinfectant; fungal infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel theta defensin analog useful for reducing or inhibiting growth survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps

    18
/note= "The peptide is cyclised by a covalent link
between these two residues"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 86;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; SEQ ID NO 3; 46pp; English.
                                                                                                                                                                                                                                                        Location/Qualifiers
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66.78;
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Best Local Similarity 66.77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18 AA;
                                                                                                                                                                                                         Macaca mulatta
                                                                                                                                                                                                                                                                                                                                                               Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                              Disulfide-bond
                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Selsted ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JAN-2004.
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The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO3527. The theta defensin analogue is useful for reducing or inhibiting growth or survival of the microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash colution), an inanimate object compatising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of growth. Thus the peptides are useful as incobistatic inhibition of growth. Thus the peptides are useful as the rapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensins have high antimiorobial activity and low haemolytic activity. The present sequence represents a Rhesus theta defensin analogue peptide.
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Monkey; Rhesus theta defensin; RTD; antimicrobial peptide; antimicrobial; antinflammatory; antibacterial; virucide; fungicide; food; conteat lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbicidaticy growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; disinfectant; fungal infection; haemolytic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel theta defensin analog useful for reducing or inhibiting growth survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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Pred. No. 0.011;
2; Mismatches
                                                                                                                                                                                                                                                                                                             Location/Qualifiers
3. .16
5. .14
7. .12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 16; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADO35241 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
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Best Local Similarity 66.7
Warches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Selsted ME, Tran DQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-167945/16.
                                                                                                                                                                                                                                                                                                                                                                                          Disulfide-bond
Disulfide-bond
Modified-site
                                                                                                                                                                                                                                Macaca mulatta.
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                                                                                                                                                                                                                                                                                                                                                            Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JAN-2004.
                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  object.
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ADO35241
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RESULT 38

defensin analogue peptide aRTD-3-OH.

(first entry)

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The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as AD035239-AD035257. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of survival of microorganisms as well as microbistatic inhibition of growth. Thus the peptides are useful as the respectic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents a Rhesus theta defensin analogue peptide.
                                                                                                                Monkey; Rhesus theta defensin; RTD; antimicrobial peptide; antimicrobial; antiinflammatory; antibacterial; virucide; fungicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition, microbistatic growth inhibition; disinfectant; food preservative; bacterial inflection; viral inflection; disinfectant; fungal inflection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-APR-2003; 2003US-00427715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                      Disulfide-bond
Disulfide-bond
Disulfide-bond
Modified-site
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                                                                                                                                                                                                                                                 Macaca mulatta
                                                                                     Rhesus theta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-APR-2002;
                                                 15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JAN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Selsted ME,
                                                                                                                                                                                                                                                                  Synthetic
                 ADO35241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          object
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Tran DQ;

/note= "Hydroxylated"

Location/Qualifiers

3. .16 5. .14 7. .12

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                                                                                                              Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV; human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; cyclic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                               amino acid at position 1 to form a
                                                                                                                                                                                                                             /note= "Linked to amino acid at position 18 to form cyclic structure"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually
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Best Local Similarity 72.2%; Pred. No. 0.014;
Matches 13; Conservative 0; Mismatches 5: Tndole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hong TB;
                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                             /note= "Linked to
cyclic structure"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE33803 standard; peptide; 18 AA
                                                                                       I15Y retrocyclin peptide analogue.
AAE33804 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lehrer RI, Waring AJ, Cole AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transmitted diseases, vaginosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 9; Page 24; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-APR-2001; 2001US-0284855P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GICKCICGRGICRCYCGR
                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                  3. .16
5. .14
7. .12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-103387/09
                                                                                                                                                                                                                                                                    Disulfide-bond 3
Disulfide-bond 5
Disulfide-bond 7
Misc-difference 1
                                                                                                                                                                                                            Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                             WO200285401-A1
                                                                                                                                                                               Unidentified
                                                         16-APR-2003
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Gaps . 0

Score 86; DB 8; Length 18; Pred. No. 0.011; 2; Mismatches 4; Indels

GVCRCLCRRGVCRCLCRR 18 1 GFCRCICTRGFCRCICTR 18

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16-APR-2003 (first entry)

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The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin-mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is human retrocyclin peptide analogue
                                                                    Retrocyclin, infection, sexually transmitted disease, gene therapy, HIV, human immunodeficiency virus; bacterial vaginosis; ophthalmic infection, antibiotic modelling; antimicrobial; cyclic.
                                                                                                                                                                             /note= "Linked to amino acid at position 18 to form a cyclic structure"
3. .16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually transmitted diseases, vaginosis.
                                                                                                                                                                                                                                                                            /note= "Linked to amino acid at position 1 to form cyclic structure"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhesus theta defensin analogue peptide RTD-5.
                                                                                                                                                           Location/Qualifiers
                                         16Y retrocyclin peptide analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9; Page 24; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADO35256 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.3%;
                                                                                                                                                                                                                                                                                                                                                                                 18-APR-2002; 2002WO-US012353
                                                                                                                                                                                                                                                                                                                                                                                                             18-APR-2001; 2001US-0284855P
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                                                                                                                                                                                                                                                                                                                                                                                                                                         (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lehrer RI, . Waring AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-103387/09.
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                                                                                                                                                           Key
Misc-difference
                                                                                                                                                                                                                                Disulfide-bond
Disulfide-bond
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18 AA;
                                                                                                                                                                                                                    Disulfide-bond
                                                                                                                                                                                                                                                                                                                       WO200285401-A1
                                                                                                                               Unidentified
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Matches
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Hong

Cole AM,

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The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO3527. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting cowth or survival of a microorganism in an environment such as food or sourtion, an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for the infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents a Rhesus theta defensin analogue peptide.
Monkey, Rhesus theta defensin, RTD; antimicrobial peptide, antimicrobial, antinflammatory; antibacterial; virucide, fungicide, food; contact lens solution, eye wash solution, inflammatory response; microbicidal inhibition, microbistatic growth inhibition; disinfectant; food preservative, bacterial infection; viral infection; disinfectant; fungal infection; haemolytic activity; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate object.
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    .18

note= "The peptide is cyclised by a covalent link

between these two residues"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 8;
0.014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 85; DB E
Pred. No. 0.014
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 30; 46pp; English.
                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                   30-APR-2003; 2003US-00427715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-APR-2002; 2002US-0377071P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.3%;
75.0%;
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Best Local Similarity 75.v.
Best Local 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GFCRCICTRGFCRCIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Selsted ME, Tran DQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-167945/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 AA;
                                                                                                                                                                                                                                                                                                     Disulfide-bond
                                                                                                                                    Macaca mulatta
                                                                                                                                                                                                                                                                 Disulfide-bond
Disulfide-bond
                                                                                                                                                                                          Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                22-JAN-2004.
                                                                                                                                                        Synthetic.
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Search completed: October 26, 2004, 15:34:54 Job time : 116 secs

GICRCLCRRGVCRCIC 16

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Gaps

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Length 18; 5; Indels

Score 85; DB 6; Pred. No. 0.014; 0; Mismatches

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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_REW PUBL_pep:*
3: /cgn2_6/ptodata/2/pubpaa/PCT_REW PUBL_pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUBL_pep:*
5: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUBL_pep:*
6: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUBL_pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUBL_pep:*
9: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUBL_pep:*
9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US106_PUBCOMB.pep:*
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19: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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19: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1364641 seqs, 323758627 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
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1 GFCRCICTRGFCRCICTR 18
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

App1	Appli	Appli	Appl	Appli	Appl	Appl	Appl	Appl	Appl	Appli	Appl	Appli	Appl	Appl	Appl	Appli	Appli	Appl	Appli	Appl	Appl	Appl	Appl	Appli	Appli	Appl	Appl	Appl	Appl	Appl
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7 - 7	-10-141-645-	US-10-313-994-9	-10	US-10-141-645-1	-83	-427	-090-	-72	US-09-917-340-53	US-10-141-645-2	-060	US-10-427-715-3	2	US-10-427-715-16	10-721-8	US-10-141-645-3	10-141	2	2	US-10-427-715-19	9	10-4	10-427-71	10-141-64	US-10-141-645-9	US-10-427-715-28	US-10-427-715-37	US-10-427-715-38	10-427-71	US-10-313-994-21
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APPLICANT: MAURY, WENDY
APPLICANT: STAPLETON, JACK
APPLICANT: STAPLETON, JACK
APPLICANT: STANSKI, MARK
APPLICANT: STANSKI, MARK
APPLICANT: MCCRAY, PAUL B.
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALII
TITLE OF INVENTION: CATHELICIDINS
TI frienty of current 18 pm ö Gaps OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Peptide US-10-060-102-28 ·, Query Match
100.0%; Score 116; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels (Sequence 28, Application US/10060102 Publication No. US20030022829A1 GENERAL INFORMATION: ORGANISM: Artificial Sequence

es 18; Conservative U; Mismatches U; In 1 GFCRCICTRGFCRCICTR 18

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1 GPCRCICTRGFCRCICTR 18

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100.0%; Score 116; DB 15; Length 18; 100.0%; Pred. No. 1e-06; tive 0; Mismatches 0; Indels 0
US-10-427-715-2
Sequence 2, Application US/10427715
Sequence 2, Application US/10427715
Publication VOSCO40014669A1
GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Tran, Dat Q.
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Thereof, and Methods of Use
FILE REPRENT Selsted, MICHAEL US/10/427,715
CURRENT PILING DATE: 2003-04-30
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO SECOND NOS: 41
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Train, Dat Q.
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Thereof, and Methods of Use
FILE REFERENCE: 66778-302 (UC5754)
FILE REFERENCE: 66778-302 (UC5754)
CURRENT FILING DATE: 2003-04-30
PRIOR PRILING DATE: 2003-04-30
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Mindows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 15;
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Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: synthetic construct US-10-427-715-14
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Publication No. US20040086535A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S-10-427-715-14 / Sequence 147-Application US/10427715 Sequence 147-Application US/10427715 Publication No. US20040014669A1 APPLICANT: Selsted, Michael E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GFCRCICTRGFCRCICTR 18
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TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Macaca mulatta
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US-10-721-839-28
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FAGE 2

**PLICANT: "MAURY, WENDY

**PLICANT: STREETON, JACK

**PAPLICANT: STREETON, JACK

**PAPLICANT: ROLLER, RICHARD

**PAPLICANT: ROLLER, RICHARD

**PAPLICANT: STINSKI, MARK

**PAPLICANT: ROLLER, MICHAR, MALK

**PAPLICANT: NOVEL NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI!

**TITLE OF INVENTION: CAPTHELICIDINS

**PLICANT: NOVEL NOVEL 1004.035US

**PLICANT: NOVEL NOVEL 1005.01.25

**PRIOR TELING DATE: 2003-01.25

**PRIOR PELICATION NUMBER: 60/309,368

**PRIOR PELICATION NUMBER: 60/306,102

**PRIOR PELICATION NUMBER: 60/306,103

**PRIO
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Sequence 32, Application US/10060102

Publication No. US20030022829A1

GENERAL INFORMATION:
APPLICANT: MAURY, WENDY
APPLICANT: STAFLETON, JACK
APPLICANT: STAFLETON, JACK
APPLICANT: STINKI, MARK
APPLICANT: TACK, BRIAN
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAWALI!
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAWALI!
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAWALI!
TITLE OF INVENTION: NOVELS: US. 1200-02-02-22
CURRENT APPLICATION NUMBER: 60/202-02-22
CURRENT FILING DATE: 2001-08-01

PRIOR PRILING DATE: 2001-08-01

PRIOR FILING DATE: 2001-08-01

PRIOR FILING DATE: 2001-08-01

PRIOR FILING DATE: 2001-08-01

SEQ ID NOS: 32

LENGTH: 18

LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: Synthetic in OTHER INFORMATION: Peptide US-10-721-839-28
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100.0%; Pred. No. 1e-06;
ive 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity
Matches 18; Conserv
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US-10-060-102-32
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Sequence 1. Application US/10313994

Sequence 1. Application US/10313994

Publication No. US20030162718A1

GENERAL INFORMATION

APPLICANT: Selsted, Winchael E.

APPLICANT: Tang, Yi-Quan

APPLICANT: Tun, Jun

APPLICANT: Outliette, Addresd.

TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
FILE REPERENCE: P-UC 3095

FILE REPERENCE: P-UC 3095

CURRENT APPLICATION NUMBER: US/10/313,994

CURRENT FILING DATE: 1999-05-10

PRIOR PLING DATE: 1999-05-10

NUMBER OF SEQ ID NOS: 31

SOFTWARE: Patentin Ver. 2.0
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Peptide
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| Sequence 1, Application US/10427715 |
| Sequence 1, Application US/10466941 |
| Sequence 1, Application US/001466941 |
| Publication No. US2004001466941 |
| APPLICANT: Selsted, Michael E. |
| APPLICANT: Tran, Dat Q. |
| TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs TITLE OF INVENTION: UNMERR: US/10/427,715 |
| CURRENT APPLICATION NUMBER: US/10/427,715 |
| PRIOR APPLICATION NUMBER: US/00/204-30 |
| NUMBER OF SEQ ID NOS: 41 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
                                                                                                                                                      Query Match 87.1%; Score 101; DB 14; Length 18; Best Local Similarity 83.3%; Pred. No. 4.8e-05; Matches 15; Conservative 1; Mismatches 2; Indels
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83.3%; Pred. No. 4.8e-05;
tive 1; Mismatches 2; Indels
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Best Local Similarity 83.33
Matches 15; Conservative
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ORGANISM: Macaca mulatta
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                                                                                   US-10-060-102-30
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US-10-313-994-1
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LENGTH: 18
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LENGTH: 18
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                                                                                                                                                                                                                                                                                                                          GENERAL INCOMACTION:
APPLICANT: MAURY, WENDY
APPLICANT: STARLETON, JACK
APPLICANT: STARLETON, JACK
APPLICANT: STINSKI, MARK
APPLICANT: STINSKI, MARK
APPLICANT: TACK, BRIAN
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI
TITLE OF INVENTION: NOVELS ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI
TITLE OF INVENTION: NOVERE: US/10/060,102
TITLE OF INVENTION NUMBER: US/10/060,102
PRIOR PELLING DATE: 2003-11-25
PRIOR PELLING DATE: 2001-08-01
PRIOR FILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 3.2
SOFTWARE: PATENTIN UNIVER: 60/265,270
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 3.2
SEQ ID NO 3.32
LENGTH: 18
THE OF THE OFFICE OF
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| Sequence 30, Application US/10060102
| Publication No. US20030022829A1
| GENERAL INFORMATION:
| APPLICANT: MAURY, WENDY
| APPLICANT: STARLETON, JACK
| APPLICANT: STINKI, MARK
| APPLICANT: STINKI, MARK
| APPLICANT: ACCENT, MAUL B.
| APPLICANT: ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI TILE OF INVENTION: NOVEL ANTIVITIES OF PRIMATE THEO DEFENSINS AND MAMMALI TILE OF INVENTION NUMBER: 06/202
| PRIOR PPLICATION NUMBER: 60/206,102
| PRIOR PLING DATE: 2001-02-02
| PRIOR PLING DATE: 2001-03-03
| PRIOR PLING DATE: 2001-03-03
| NUMBER OF SEQ ID NOS: 32
| SOFTWARE: PatentIN Ver: 2.1
| SEQ ID NO 30
| LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Synthetic COTHER INFORMATION: Peptide US-10-721-839-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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88.8%; Score 103; DB 15; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.9e-05;
Matches 16; Conservative 0; Mismatches 2; Indels
                                                                                                                                                          RESULT 6
10S-10-721-839-32
Sequence 32, Application US/10721839
Publication No. US20040086535A1
GENERAL INFORMATION:
1 GFCRCICTRGFCRCICTR 18
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APPLICANT: Tran, 0, 101 Q.
ITILE OF INVENTION: Antimicrobial Theta Defensins, Analogs
ITILE OF INVENTION: Antimicrobial Theta Defensins, Analogs
ITILE OF INVENTION: Thereof, and Methods of Use
FILE REPERSONCE: 65778-302 (UG5754)
CURRENT APPLICATION NUMBER: US/10/427,715
CURRENT RILING DATE: 2003-04-30
PRIOR PILING DATE: 2003-04-30
NUMBER: OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 101; DB 15;
Pred. No. 4.8e-05;
0; Mismatches 2;
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GENERAL INFORMATION:
APPLICANT: STAPLETON, JACK
APPLICANT: SCILLER, RICHARD
APPLICANT: STINSKI, MARK
APPLICANT: STINSKI, MARK
APPLICANT: MCCRAY, PAUL B.
APPLICANT: TACK, BRIAN
                                                            ; Sequence 24, Application US/10427715; Publication No. US20040014669A1
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ORGANISM: Artificial Sequence
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                                                                                                         GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
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Best Local Similarity 88.99
Matches 16; Conservative
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0
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APPLICANT: Tran, Dat Q.
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Thereof, and Methods of Use
FILE REFERENCE: 66778-302(UC5754)
CURRENT APPLICATION NUMBER: US/10/427,715
CURRENT FILING DATE: 2003-04-30
PRIOR APPLICATION WUMBER: US 60/377,071
PRIOR PILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 41
SOTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13, Application US/10427715
Publication No. US20040014669A1
FUBLICATION No. US20040014669A1
APPLICANT: Selsted, Michael E.
APPLICANT: Tran, Dat O.
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Thereof, and Methods of Use
FILE REPERENCE: 66778-302 (UGS754)
CURRENT APPLICATION NUMBER: US/10/427,715
CURRENT FILING DATE: 2003-04-30
PRIOR FILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 87.1%; Score 101; DB 15; Length 18; Best Local Similarity 83.3%; Pred. No. 4.8e-05; Matches 15; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 83.3%; Pred. No. 4.8e-05;
Matches 15; Conservative 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: synthetic construct US-10-427-715-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: synthetic construct
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LOCATION: 18
COTER INFORMATION: at the C terminus
US-10-427-715-13
                                                                                              US-10-427-715-12
Sequence 12, Application US/10427715
Publication No. US20040014669A1
GENERAL INFORMATION:
1 GFCRCLCRRGVCRCICTR 18
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Length 18;

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TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALIFIED OF INVENTION: CATHELICIDINS
TITLE OF INVENTION: CATHELICIDINS
THE REPERBANCE: 100A-035US
CURRENT APPLICATION NUMBER: US/10/721,839
CURRENT FILING DATE: 2003-11-25
PRIOR FILING DATE: 2003-02-2
PRIOR FILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
SOFTWARE PLING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 30
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: Description of Artificial Sequence:
) OTHER INFORMATION: Peptide
US-10-721-839-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GFCRCLCRRGVCRCICTR 18
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US-10-141-645-6

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US-10-427-715-29
Sequence 29, Application US/10427715
Sequence 29, Application US/10427715
Sequence 29, Application US/10465941
GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Tran, Dat Q.
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Thereof, and Methods of Use
FILE REPREDRATE 5070 (UCS754)
CURRENT APPLICATION NUMBER: US/10/427,715
PRIOR PILING DATE: 2003-04-30
NUMBER OF SEQ ID NOS: 41
SEQ ID NOS: 41
LENGTH: 18
LENGTH: 18
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86.2%; Score 100; DB 15; Length 18;

Best Local Similarity 93.8%; Pred. No. 6.2e-05;

Matches 15; Conservative 0; Mismatches 1; Indels
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APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REPERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: 60/284,855
PRIOR FILING DATE: 2001-04-18
FRIOR FILING DATE: 2001-04-18
FRIOR PELING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO
SEQ ID NOS: LENGTH: LENG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GFCRCICTRGFCRCICTR 18
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US-10-141-645-5
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RESULT 16

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Publication No. US20030162718A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Tang, Yi-Quan
APPLICANT: Yuan, Jun
APPLICANT: Outlette, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same;
FILE REFRENCE: PUC 3095
CURRENT APPLICATION NUMBER: US/09/313,994
CURRENT FILING DATE: 2002-12-05
PRIOR APPLICATION NUMBER: US/09/309,487
PRIOR PILING DATE: 1999-05-10
NUMBER OF SEQ 1D NOS: 31
SOFTHARE: PATENTIN VEY: 2.0
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Sequence 6, Application US/10141645;
Publication No. US20030144184A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alexander Cole
APPLICANT: Arexander Cole
APPLICANT: Arexander Cole
APPLICANT: Arexander Cole
APPLICANT: Arexander Cole
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT FILING DATE: 2002-05-06
PRIOR PILING DATE: 2001-04-18
PRIOR PILING DATE: 2001-04-18
PRIOR PILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SEQ TWARE: FARCESQ for Windows Version 4.0
SEQ TUBNET: 18
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80.2%; Score 93; DB 14;
Best Local Similarity 77.8%; Pred. No. 0.00038;
Matches 14; Conservative 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: synthetic variant US-10-141-645-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 81.24
Matches 13; Conservative
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US-10-313-994-9
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US-10-060-102-27
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LENGTH: 18
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GENERAL INFORMATION:
APPLICANT: MAURY WENDY
APPLICANT: STABLETON, JACK
APPLICANT: STABLETON, JACK
APPLICANT: STABLETON, JACK
APPLICANT: STINSKI, MARK
APPLICANT: TACK, BRIAN
ITLE OF INVENTION: CATHELICIDINS
ITLE OF INVENTION: CATHELICIDINS
FILE REPERRNCE: 10WA:035US
CURRENT APPLICATION NUMBER: US/10/721,839
CURRENT APPLICATION NUMBER: US/10/060,102
PRIOR PILING DATE: 2002-02-2
PRIOR PILING DATE: 2001-08-01
PRIOR PILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NOS: 32
SOFTWARE: PATENTIN VEY: 2.1
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic;

OTHER INFORMATION: Peptide
US-10-721-839-27
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Pred. No. 0.00081;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
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Sequence 23, Application US/10427715

Sequence 23, Application US/10427715

PUBLICANT: Selsted, Michael E.

APPLICANT: Selsted, Michael E.

APPLICANT: Selsted, Michael E.

APPLICANT: Dat Q.

TITLE OF INVENTION: Antimicrobial Theta Defensins, F.

TITLE OF INVENTION: Antimicrobial Theta Defensins, F.

TITLE OF INVENTION: Thereof, and Methods of Use, F.

TITLE OF INVENTION: Thereof, and Methods of Use, F.

TITLE OF INVENTION: Thereof, and Methods of Use, F.

FILE REPERENCE: 66778-302 (UC5754)

CURRENT APPLICATION NUMBER: US/10/427,715

PRIOR PILING DATE: 2003-04-30

NUMBER OF SEQ ID NOS: 41

SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Artificial Sequence
                     Publication No. US20040086535Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 77.8
Matches 14; Conservative
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Best Local Similarity
Matches 14; Conserv
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LENGTH: 18
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APPLICANT: MAURY, WENDY
APPLICANT: STAPLETON, JACK
APPLICANT: STAPLETON, JACK
APPLICANT: STAPLETON, JACK
APPLICANT: STANKI, MARK
APPLICANT: STINKI, MARK
APPLICANT: ATRICK, BRIAN
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI
TITLE OF INVENTION: CATHELICIDINS
TITLE OF INVENTION: CATHELICIDINS
TITLE OF INVENTION: CATHELICIDINS
FILE REFERRINCE: 100A-03-50S
CURRENT APPLICATION NUMBER: 60/309,368
PRIOR PILING DATE: 2001-08-01
PRIOR PAPLICATION NUMBER: 60/265,270
PRIOR PAPLICATION NUMBER: 60/265,270
PRIOR PILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 32
SOFITANE: PALENTING VET: 2.1
SEQ ID NO 27
LENGTH: 18
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Pred. No. 0.00081;
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Publication No. US20030144184A1
GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral
TITLE OF INVENTION: Antimicrobial Peptides
TITLE OF INVENTION: Antimicrobial Peptides
TITLE OF INVENTION: Antimicrobial Peptides
TITLE OF INVENTION NUMBER: US/10/141,645
CURRENT FILING DATE: 2002-05-06
PRIOR PHILOATION NUMBER: 60/284,855
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 77.8%;
Matches 14; Conservative
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US-10-141-645-1
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Best Local Similarity
Matches 14; Conserv
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US-10-141-645-1
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LENGTH: 18
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1 GFCRCRRGVCLCICTR 18

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RESULT 22

RESULT 20 US-10-721-839-27 Sequence 27, Application US/10721839 ö

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Gaps
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75.0%; Score 87; DB 9; Length 18;
Best Local Similarity 86.7%; Pred. No. 0.0018;
Matches 13; Conservative 1; Mismatches 1; Indels
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Publication No. US20030144184A1

GENERAL INFORMATION:

APPLICANT: Robert Lehrer

APPLICANT: Alan Waring

APPLICANT: Alexander Cole

APPLICANT: Teresa Hong

TITLE OF INVENTION: Retrocyclins - Antiviral and

TITLE OF INVENTION: Antimicrobial Peptides

TITLE OF INVENTION: Antimicrobial Peptides

TITLE REFERENCE: 2002-05-06

CURRENT FILING DATE: 2002-05-06

PRIOR APPLICATION NUMBER: US/10/141,645

CURRENT FILING DATE: 2001-04-18

FRIOR APPLICATION NUMBER: Unassigned

PRIOR APPLICATION NUMBER: Unassigned

PRIOR FILING DATE: 2002-04-18

NUMBER OF SEQ ID NOS: 125

SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 0.0018;
Best Local Similarity 72.2%; Pred. No. 0.0014;
Matches 13; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: MUTDHY, Christopher J.
APPLICANT: MoAnulty, Jonathan F.
TILE OF INVENTION: Transplant Media
FILE REPERRICE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT FILING DATE: 2001-07-29
PRIOR APPLICATION NUMBER: 60/221,632
PRIOR PILING DATE: 2000-07-28
PRIOR PILING DATE: 2000-11-17
PRIOR PILING DATE: 2000-11-17
PRIOR PILING DATE: 2000-11-17
PRIOR PILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SEQ ID NO 53
LENGTH: 18
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                   US-09-917-340-53
, Sequence 53, Application US/09917340
; Patent No. US20020090369A1
; GENERAL INFORMATION:
                                                                                                       1 GFCRCICTRGFCRCICTR 18
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Best Local Similarity
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LENGTH: 18
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| Sequence 31, Application US/20040086535A1
| Sequence 31, Application No. US20040086535A1
| GENERAL INFORMATION:
| APPLICANT: MAUNY, WENDY
| APPLICANT: STAREFOW, JACK
| APPLICANT: STINKI, MAKK
| APPLICANT: ROLLER, RICHARD
| APPLICANT: ROLLER, RICHARD
| APPLICANT: ROLLER, RICHARD
| APPLICANT: MACK, MAKK
| APPLICANT: WCRAY, PAUL B.
| TITLE OF INVENTION: CAPHELICIDINS
| TITLE OF INVENTION: CAPHELICIDINS
| FILE REFERENCE: 100A-105-12
| FRIOR APPLICATION NUMBER: US/10/060,102
| PRIOR FILING DATE: 2001-01-30
| PRIOR FILING DATE: 2001-01-30
| PRIOR FILING DATE: 2001-01-30
| WUMBER OF SEQ ID NOS: 32
| SEQ ID NO 31
| LEASTH APPLICATION NUMBER: 60/265,270
| WUMBER OF SEQ ID NOS: 32
| SEQ ID NO 31
| LEASTH APPLICATION NUMBER: MCRAY BRIGHT APP
                  Sequence 31, Application US/10060102

Publication No. US20030022829A1

GENERAL INFORMATION:

APPLICANT: MAURY, WENDY

APPLICANT: ROLLER, RICHARD

APPLICANT: STINKI, MARK

APPLICANT: ROLLER, RICHARD

TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI

TITLE OF INVENTION: CATHELICIDINS

FILE REFERENCE: 100MA:035US

CURRENT APPLICATION NUMBER: 60/309,368

PRIOR APPLICATION NUMBER: 60/265,270

PRIOR PELING DATE: 2001-01-30

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PATENTIN VOY: 2.1

SEQ ID NO 31

LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Peptide
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Pred. No. 0.0014;
1; Mismatches 4; Indels
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Best Local Similarity 72.2%;
Matches 13; Conservative
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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           US-10-060-102-31
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Sequence 16, Application US/10427715
Sequence 16, Application US/10427715
Sequence 16, Application O. US20040014669A1
Septication No. US20040014669A1
APPLICANT: Tran, Dat Q.
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Antimicrobial Thereof, and Methods of Use
CURRENT APPLICATION WUMBER: US/10/427,715
SPIOR APPLICATION NUMBER: US 60/377,071
PRIOR PILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5502
LENGTH: 18
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Pred. No. 0.0023;
2; Mismatches 4; Indels
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                                                                                                                                                                                                                                           APPLICANT: Selected, Michael E.
APPLICANT: Selected, Michael E.
APPLICANT: Tran, Dat Q.
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Thereof, and Methods of Use FILE REFERENCE: 66778-302(UCS754)
CURRENT APPLICATION NUMBER: US/10/427,715
CURRENT FILING DATE: 2003-04-30
PRIOR PLING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 18
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LOCATION: 18
COTHER INDOMATION: at the C terminus
US-10-427-715-16
                                                                                                                                             US-10-427-715-15
Sequence 15, Application US/10427715
Publication No. US20040014669A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 66.7%;
Matches 12; Conservative
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                              APPLICANT: MACRY, WENDY
APPLICANT: STAPLETON, JACK
APPLICANT: STAPLETON, JACK
APPLICANT: STAPLETON, JACK
APPLICANT: STINSKI, MARK
APPLICANT: STINSKI, MARK
APPLICANT: TACK, BRIAN
TILE OF INVENTION: OVTHELLIDINS
TITLE OF INVENTION: CATHELLIDINS
TITLE OF INVENTION: CATHELLIDINS
TITLE OF INVENTION: OVARIBER: US/10/060,102
CURRENT APPLICATION NUMBER: 60/309,368
PRIOR FILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 32
STONMER PROPERTY OF THE TOWN NOSE OF THE TOWN NUMBER: 60/265,270
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 32
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Gaps
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Bublication No. US20040014669A1

GENERAL INFORMATION:

APPLICANT: Selsted, Michael B.

APPLICANT: Tran, Dat Q.

TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs

TITLE OF INVENTION: Thereof, and Methods of Use

FILE REFERENCE: 66778-302 (UC5754)

CURRENT APPLICATION NUMBER: US 60/377,715

CURRENT PILING DATE: 2003-04-30

PRIOR APPLICATION NUMBER: US 60/377,71

PRIOR APPLICATION NUMBER: US 60/377,71

SEQ ID NO 3

LENGTH: 18

LENGTH: 18

TYPE: PRICE ANGER MAGGE MINDOWS VERSION 4.0

SEQ ID NO 3

LENGTH: 18

TYPE: PRICE MAGGE MULDICA
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Indels
  4;
  Mismatches
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Sequence 29, Application US/10060102
Publication No. US20030022829A1
GENERAL INFORMATION:
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                                                                                                1 GICRCICGKGICRCICGR 18
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ORGANISM: Artificial Sequence
FEATURE:
                                                  1 GPCRCICTRGFCRCICTR
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  13; Conservative
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Matches 12; Conserva
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| Sequence 30, Application US/10427715 |
| Sequence 30, Application WS/10427715 |
| Sequence 30, Application No. USC040014669A1 |
| GENERAL INFORMATION: |
| APPLICANT: Selsted, Michael E. |
| APPLICANT: Tran, Dat Q. |
| TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs |
| TITLE OF INVENTION: Thereof, and Methods of Use |
| TITLE OF INVENTION: Thereof, and Methods of Use |
| TITLE OF INVENTION: Thereof, and Methods of Use |
| TITLE OF INVENTION: Thereof, and Methods of Use |
| TITLE OF INVENTION: WINBER: US/10/427,715 |
| CURRENT APPLICATION NUMBER: US 60/377,071 |
| PRIOR PILING DATE: 2002-04-30 |
| NUMBER OF SEQ ID NOS: 41 |
| SOFTWARE: PASSEQ for Windows Version 4.0 |
| SEQ ID NO 30 |
| LENGTH: 18
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Best Local Similarity 75.0%; Pred. No. 0.0029;
Matches 12; Conservative 1; Mismatches 3; Indels
                                     Indels
                                                                                                                                                                                                                                                                                                                              US-10-141-845-4

Publication No. US20030144184A1

GENERAL INFORMATION:

APPLICANT: Robert Lehrer

APPLICANT: Robert Lehrer

APPLICANT: Alan Waring

APPLICANT: Alexander Cole

APPLICANT: Teresa Hong

ITILE OF INVENTION: Retrocyclins - Antiviral

TILE OF INVENTION: Antimicrobial Peptides

TILE OF INVENTION: Antimicrobial Peptides

TILE OF INVENTION: Antimicrobial Peptides

FILE REFERENCE: UCLA-001CIP

CURRENT APPLICATION NUMBER: US/10/141,645

CURRENT FILING DATE: 2002-05-06

PRIOR FILING DATE: 2001-04-18

PRIOR APPLICATION NUMBER: 60/284,855

PRIOR FILING DATE: 2002-04-18

NUMBER OF SEC ID NOS: 125

SEOTHARE: FastSEQ for Windows Version 4.0

SEOTHARE: LEMETHER DESCRIPTION NUMBER: LEMETHER DESCRIPTION NUMBER: MINGOWS VERSION 4.0
Best Local Similarity 72.2%; Pred. No. 0.0029;
Matches 13; Conservative 0; Mismatches 5;
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, OTHER INFORMATION: synthetic construct US-10-427-715-30
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                                                                                                        1 GFCRCICTRGFCRCICTR 18
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                                                                                                                Sequence 29, Application US/10721839
Publication No. US20040086535A1
GENERAL INFORMATION:
APPLICANT: STAPLETON, JACK
APPLICANT: STAPLETON, JACK
APPLICANT: STAPLETON, JACK
APPLICANT: TACK: RAIAN
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI
TITLE OF INVENTION NOVELS: 105/10/206,102
PRIOR PLING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 29
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TENERAL PRIMATE PRIMATE THETA DEFENSINS
SEQ ID NO 29
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COTHER INFORMATION: Description of Artificial Sequence: Synthetic
COTHER INFORMATION: Peptide
US-10-721-839-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/10141645
Publication No. US200301441841
GENERAL INFORMATION:
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Teresa Hong
IITLE OF INVENTION: Retrocyclins - Antiviral and
IITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-001CIP
CURRENT FILING DATE: 2002-05-06
FRIOR FILING DATE: 2001-04-18
FRIOR FILING DATE: 2001-04-18
FRIOR FILING DATE: 2002-04-18
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; OTHER INFORMATION: synthetic variant
US-10-141-645-3
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ORGANISM: Artificial Sequence
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Best Local Similarity 66.74
Matches 12; Conservative
                                                               RESULT 30
US-10-721-839-29
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LENGTH: 18
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NAME/KEY: AMIDATION
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TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Antimicrobial Methods of Use
TITLE OF INVENTION: Thereof, and Methods of Use
TITLE OF INVENTION: Thereof, and Methods of Use
TITLE OF INVENTION NUMBER: US/10/427,715
CURRENT PILING DATE: 2003-04-30
PRICR FLING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 71.6%; Score 83; DB 15; Length 18; Best Local Similarity 72.2%; Pred. No. 0.0049; Matches 13; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 83; DB 14; Length 18;
Pred. No. 0.0049;
0; Mismatches 5; Indels
                                                                                                                                                          Sequence 7, Application US/10141645

Publication No. US20030144184A1

GENERAL INFORMATION:

APPLICANT: Alow Maxing

APPLICANT: Alow Maxing

APPLICANT: Alexander Cole

CURRENT APPLICATION NUMBER: US/10/141,645

CURRENT FILING DATE: 2002-05-06

PRIOR APPLICATION NUMBER: Unassigned

PRIOR FILING DATE: 2002-04-18

PRIOR FILING DATE: 2002-04-18

SOFTWARE FREESE FASTSED for Windows Version 4.0

SEQUENCY
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CTHER INFORMATION: synthetic variant
US-10-141-645-7
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, Sequence 19, Application US/10427715
, Publication No. US20040014669A1
, GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
1 GFCRCICTRGFCRCIC 16
                                1 GICRCLCRRGVCRCIC 16
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Best Local Similarity 72.2%;
Matches 13; Conservative
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Sequence 20, Application US/10427715
; Sequence 20, Application US/10427715
; Publication No. US20040014669A1
; GENERAL INFORMATION:
; APPLICANT: Seleted, Michael E.
APPLICANT: Tran, Dat Q.
; TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Thereof, and Methods of Use
FILE REFERENCE: 66778-302 (UC5754)
; CURRENT APPLICATION NUMBER: US 60/377,071
PRIOR APPLICATION NUMBER: 2003-04-30
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PASLESEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17, Application US/10427715

Sequence 17, Application US/10427715

Publication No. US20040014669A1

GENERAL INFORMATION:

APPLICANT: Selsted, Michael E.

APPLICANT: Tran, Dat Q.

TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Thereof, and Methods of Use

FILE REFERENCE: 66778-302 (UC5754)

CURRENT APPLICATION NUMBER: US/10/427,715

CURRENT FILING DATE: 2003-04-30

PRIOR FILING DATE: 2002-04-30

NUMBER OF SEQ ID NOS: 41

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70.7%; Score 82; DB 15; Length 18; 68.8%; Pred. No. 0.0064; tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
71.6%; Score 83; DB 15; Length 18;
Best Local Similarity 72.2%; Pred. No. 0.0049;
Matches 13; Conservative 1; Mismatches 4; Indels
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; OTHER INFORMATION: at the C terminus
US-10-427-715-17
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ORGANISM: Artificial Seguence
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Best Local Similarity 68.8
Matches 11; Conservative
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RESULT 38

1 GFCRALCRRGVCRAICTR 18

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US-10-427-715-31

Sequence 31, Application US/10427715

Publication No. US20040014669A1

GENERAL INFORMATION:

APPLICANT: Selsted, Michael E.

APPLICANT: Tran, Dat Q.

TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
CURENT APPLICATION WOMBER: US/10/427,715

CURENT FILING DATE: 2003-04-30

PRIOR FILING DATE: 2002-04-30

NUMBER OF SEQ ID NOS: 41

SOUTHARE: PastSEQ for Windows Version 4.0

SEQ ID NO 31

LENGHH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 70.7%; Score 82; DB 15; Length 18; Best Local Similarity 75.0%; Pred. No. 0.0064; Matches 12; Conservative 0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-1U-11-045-8

Deblication No. US20030144184A1

FUNDICATION NO. US20030144184A1

GENERAL INFORMATION:

APPLICANT: Alan Waring

APPLICANT: Alan Waring

APPLICANT: Alan Waring

APPLICANT: Teresa Hong

ITILE OF INVENTION: Retrocyclins - Antiviral and

ITILE OF INVENTION: Antimicrobial Peptides

TILE APPLICANT: Antiviral and

TILE OF INVENTION: Antimicrobial Peptides

FILE REPRENCE: 100.20-05-06

CURRENT APPLICATION NUMBER: 0/284,855

PRIOR FILING DATE: 2002-06-06

PRIOR FILING DATE: 2002-06-06

PRIOR FILING DATE: 2002-06-08

NUMBER OF SEQ ID NOS: 125

SOUTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8

LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
// OTHER INFORMATION: synthetic construct
US-10-427-715-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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Sequence 9, Application US/10141645; Publication No. US20030144184A1

RESULT 40 US-10-141-645-9

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GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alexander Cole
APPLICANT: Alexander Cole
APPLICANT: Alexander Cole
APPLICANT: Tereaa Hong
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-001C19
FILE REPRENCE: UCLA-0118
FRICH APPLICATION NUMBER: 60/284,855
FRIOR APPLICATION NUMBER: 60/284,855
FRIOR APPLICATION NUMBER: 108/108
FRICH APPLICATION NUMBER: 108/108
FRICH REPRENCE: TeatSEQ for Windows Version 4.0
FRICH REPAIRS: FastSEQ for Windows Version 4.0
FRATURE: TEATURE:
FRATURE: ORGANISM: Artificial Sequence
FRATURE: CALL SIMILATILY 66.7%; SCOVE 75; DB 14; Length 18;
COTHER INFORMATION: SYNTHETIC VARIANT
US-10-141-645-9

QUETY MATCH
BEST LOCAL SIMILATILY 66.7%; Pred. No. 0.039; G; Indels

QUETY MATCHES 12; CORBETVATIVE
FRATURE:
FRATURE: ARTICLE OCTURE 18
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model Run on:

October 26, 2004, 15:13:56 ; Search time 128.5 Seconds (without alignments) 80.597 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-009-317A-32 116 1 GFCRCICTRGFCRCICTR 18

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 segs, 575374646 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	mac	maca	Q6p8t4 mus musculu	Q8ch20 mus musculu	Q9d9i2 mus musculu	Aah61079 mus muscu	Q9d4k2 mus musculu						Q7seq2 neurospora		Q22048 caenorhabdi	Q95qy1 caenorhabdi		Q17641 caenorhabdi	당	Bad13491 chlamydom	Bad13492 chlamydom	Q75n88 homo sapien	Bad16738 homo sapi	075n87 homo sapien	Bad16739 homo sapi	Q7pj70 anopheles g	Q94uz6 leishmania	Q6ry99 rattus norv	72 ratt	Q9pyg3 xestia c-ni	Q7qbv4 anopheles g
SUMMARIES	9	P82270	Q9TU01	Q6P8T4	Q8CH20	Q9D9I2	AAH61079	Q9D4K2	Q949G1	Q8VJ20	Q9BLJ1	096282	YO70 NPVAC	Q7SEQ2	Q9NRB6	Q22048	Q95QY1	Q18238	017641	Q75NZ5	BAD13491	BAD13492	Q75N88	BAD16738	Q75N87	BAD16739	075770	Q94UZ6	Q6RY99	AAR24072	Q9PYQ3	Q7QBV4
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## ALIGNMENTS

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2 5	01-MAY-2000	(TrEMBLrel			Created)					
Ę	01-MAY-2000	_				sequence update)	pdate)			
ĽΩ		(TrEMBLrel	rel.		Last anno	tation	annotation update)			
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3 5	Mammalia. Entheria:	terazoa;	Drimates.	מין די מין די		ini or	erconit,	O.		
3 6	Cerconitherinae: Macaca	ew . den	ות נית נית	)		ì	1 4 )			
3 8	NCBI Tax TD-9544.	5544.	5							
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RC	TISSUE=Bone marrow,	marrow,	and	Ceuk	Leukocyte;					
ΣX	MEDLINE=99453140; PubMed=10521339	53140; E	'ubMed	=105	21339;				1	
Z.	Tang YQ.,	Yuan J.	, Oesc	apay	G., Oesa	pay K.	, Tran I	o., Milio	er C.J	
A E	Obellette A.J., Selsted M.E.; "% Chalia autimicanhis! Deatide Drodined in Drimete Lemborates	otimior	Sted r	2 C	de brodu	. 500	Drimote	T.O. T.O.	0 0 17	אין דאף
1 E	Ligation of	TWO THE	ncate	1 e 1	of Two Truncated alpha-Defensins.":	sins."	,	)	2	,
Z.	Science 286:	498-502	(1999)							
ខ្ល	-!- FUNCTION: Microbicidal activity against Gram-positive bacteria	1: Micro	bicide	al a	ctivity a	gainst	Gram-po	sitive ]	pacte:	ria
ខ្ល	S.aureus and L.monocytogenes,	s and L.	monocy	ytogi	enes, Gra	m-nega	Gram-negative bacteria	teria S	typh.	S.typhimurium
ខ្ល	and E.coli ML35	oli ML35	and	fung	and fungi C.albicans	ans and		C.neoformans	in vi	vitro.
Ņ,	-!- SUBUNIT:	Hetero	dimer	벙	SUBUNIT: Heterodimer of subunit A and subunit	and s	ubunit E	B linked by	ру	
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2	EMBL: AF191102:		AAF04391.1:		· ,•					
8	PIR: A59089;	A59085								
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H	GO; GO:0006805; P:xenobiotic metabolism;	305; P:x	enobic	otic	metaboli	sm; IEA	Α.			
DR.	InterPro; II	PR002366	; Def	ensi	n propep.					
DR	Pfam; PF0087	PF00879; Defensin propep; 1.	nsin	prop	ep; 1.					
<u>₹</u>	Antibiotic;	Defensin; Fungicide;	n; Fu	ngic	ide; Signal	al. -				
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SS		76 AA;	42	MM;	BEA207932A030590	2A0305	90 CRC64;	•		
ő	Ouery Match		55.2%;	36	Score 64;	DB	2; Length	gth 76;		
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
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MEDLINE=69279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Mish-Efficiency full-length cDNA (1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Basic protein CKT1R3.
Name=4931420D14Rik; Synonyms=Ckt1r3;
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01-JUN-2001 (TrEMBLrel. 17, Created)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 AA;
                                                                                                                                                                                                       Local Similarity
                                      SEQUENCE FROM N.A. TISSUE=Testis;
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleron M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toobhyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McZwan P.J., McKernan X.J., Mahek J.A., Guabarare P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Mizny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecidae;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Zhao C., Nguyen T., Lehrer R.I.;

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF18413, AAR07924.1;

GO, GO:0006952; P:defense response; IEA.

InterPro; IPR002366; Defensin_propep.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam, PF00879; Defensin proper; 1. SEQUENCE 76 AA; 8212 MW; 1EB307932A031826 CRC64;
                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Last annotation update)
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                                                             65 RCICTRGFCRLL 76
                                                                                                                                                     PRELIMINARY;
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Mus musculus (Mouse)
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01-MAY-2000
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Q6P8T4;
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01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:1700065105 product:hypothetical Cysteine-rich region
containing protein, full insert sequence.
Name=4931420D14Rik;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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STRAIN=CD-1; TISSUG=Testis;
Xu X., Bai X., Silvius D., Escalier D., McFarland L., Xu P.-X.;
Xu X., Bai X., Silvius D., Escalier D., McFarland L., Xu P.-X.;
Submitted (DFC) to the EMBL/GenBank/DDBJ databases.
EMBL; AF465502; AAO15675.1; -.
MGD; MGI:1913992; 4931420D14Rik.
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                                                                                                                                                                                            Length 168;
Strausberg R.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC061079; AAH61079.1; -.
Hypothetical protein.
SEQUENCE 168 AA; 18947 MW; BOOFD3D27B9BF768 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18957 MW; 8F30D3D27B9BF595 CRC64;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                            Score 59; DB 2;
Pred. No. 3;
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56.2%; Pred. No. 3;
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A STANDENGELEUELL, Shennen C.M., Schuler G.D., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., A Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marchaina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E., Rapleton M.J., Usdin T.B., Donaldo M.F., Casavant T.L., Scheetz T.E., Rapleton M.J., Usdin T.B., Peters G.J., Abramson R.D., Mullahy S.J., Rownstein M.J., Webwan P.J., McKernan K.J., Malmany S.J., Rohards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Whiting M., Nadan A., Young A.C., Shevchenko Y., Bouffard G.G., Whiting M. I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S., Jones S.J., Marra M.A.;

Rayminski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B., Addens L.D., Dickson M.C., Addens L.D., Myers R.M., Butterfield W.S., M. A., Manner M.A., Jones S.J., Marra M.A., Thuman M.A., Jones L.D., Schner Ch. M., Schein J.B., M. A., Manner M.A., Jones S.J., Marra M.A., Thuman M.A., Manner M.A., Manner M.A., Manner M.A., 
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4931420D14 product:hypothetical Cysteine-rich region
Containing protein, full insert sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                             Craniata; Vertebrata; Buteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.; Strausberg R.; Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC06.1079; AAH61079.1; -. Hypothetical_protein. Hypothetical_protein. SEQUENCE 168 AA; 18947 MW; B00FD3D27B9BF768 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sci. U.S.A. 99:16899-16903(2002).
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MEDLINE-99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
Mitho-efficiency full-length CDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
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MEDLINE-21085660; PubMed=11217851;
Hypothetical protein.
Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 CRCICTRGFCRCICTR 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA sequences."
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Best Local Similarity 56.2'
Matches 9; Conservative
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                                                                                                                                                                                                                              FROM N.A.
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09D4K2
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0
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STRAIN=CS7BL/6J; TISSUE=Testis;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I will Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length CDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Testis;
MEDILINE=20499374; PubMed=11042159;
MEDILINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Moymalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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STRAIN-C5-FECOM N.A.
STRAIN-C5-FECOM S., Akimura T., Arai A., Aono H.,
Arakawa T., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramcto K., Hiracka T., Kato H.,
Kawai J., Kojima Y., Tohno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Numazaki R., Numazaki R., Numazaki R., Numazaki R., Numazaki R., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUB=Testis; MEDLINE=20530913; PubMed=11076861; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Itashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashinwagi K., Yoneda Y., Ishikwa T., Coawa K., Tanaka T., Matsunia B., Watahiki M., Poneda Y., Ishikwa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rike integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
            SEQUENCE FROM N.A.
STRAIN=CSTBL/60; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM CONSORTIUM;
"FUNCTIONAL annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
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Muramatsu M., Hayashizaki Y.,
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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168 AA; 18931 MW; 7AZBD279612A5E94 CRC64;
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AAH61079;
14-APR-2004 (TrEMBLrel. 27, Created)
14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
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MGD; MGI:1913992; 4931420D14Rik.
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Best Local Similarity 56.4.
- المالية الم
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RESULT 6 AAH61079

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STRAIN=CDC 1551 / Oshkosh,
MEDLINE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Elsen J.A., Carpenter L., White O.,
Fleischmann R.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,
Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,
Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M.,
Fraser C.M.,
                                                                                                                                                                                                                                    Volckaert G., Pohl T.,
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE=21329048; PubMed=11435398;

MEDLINE=21329048; PubMed=11435398;

Mayer K., Murphy G., Tarchini R., Wambutt R., Volckaert G., Pohl T.

Duesterhoeft A., Stiekema W., Entian K.D., Terryn N., Lemcke K.,

Haase D., Hall C.R., van Dodeweerd A.M., Tingey S.V., Mewes H.W.,

Bevan M., Bancroft I.;

"Conservation of microstructure bewtween a sequenced region of the
genome of rice and multiple segments of the genome of Arabidopsis
thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 163;
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.9%; Score 59; DB 2; Length 274; 66.7%; Pred. No. 4.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Res. 11:1167-1174(2001).
EMBL; AJ307662; CAG39030.1; -.
Gramene; Q949G1; -.
Hypothetical protein.
SEQUENCE 274 AA; 28657 WW; ABS47D9BD5470AEI CRC64;
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Pred. No. 6;
3; Mismatches
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J. Bacteriol. 184:5479-5490(2002),
EMBL; AE007152; AAK47795.1; -.
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Best Local Similarity 60.0
Matches 9; Conservative
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                                                                                                      NCBI_TaxID=4530;
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01-MAR-2002
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Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakwar T., Bono H., Carninoi P., Pukuda S., Fukunishi Y., Furuno M.,
Hanaqaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Koya S., Kurihara C.,
A Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
A Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
A Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
R EMBL, AKO16467; BAB30253.1,
                                                                                                                                                                                                                          the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes:";
Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUB=Testis;
MEDLINE=20530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Kaisunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watsumi M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rokazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                               "Functional annotation of a full-length mouse cDNA collection.", Nature 409:685-690(2001).
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SEQUENCE 173 AA; 19581 MW; 147B6F155AC29FDF CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein C15ERIPDM.
Name=C15ERIPDM;
Oryza sativa (Rice).
                                                                                                                           SEQUENCE FRÔM N.A.
STRAIN=CS7BL/6J; TISSUE=Testis;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 CRCICTRGFCRCICTR 18
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Matches 9; Conservative
FANTOM Consortium;
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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PRELIMINARY;

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RESULT 10 Q9BLJ1

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SEQUENCE FROM N.A.
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Gardner M.J., Tettelin H., Carucci D.J., Cummings L.M., Aravind L.,
Koonin E.V., Shallom S., Mason T., Yu K., Fujii C., Pederson J.,
                                                                                     Name=C1-metal;
Ciona intestinalis.
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
NCBI_TaxID=7719;
                                                                                                                                                                                                                                                                                                     genes that are expressed during
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                       R GO; GO: 0005556; C: extracellular; IEA.

GO; GO: 0005509; C: calcium ion binding; IEA.

GO; GO: 0005509; F: calcium ion binding; IEA.

GO; GO: 0005509; F: calcium ion binding; IEA.

GO; GO: 0005509; F: chemokine activity; IEA.

GO; GO: 0005599; F: chemokine receptor activity; IEA.

GO; GO: 0005596; F: bilood coagulation; IEA.

GO; GO: 0005596; P: bilood coagulation; IEA.

GO; GO: 0005596; P: bilood coagulation; IEA.

GO; GO: 0005596; P: bilood coagulation; IEA.

R InterPro; IPR001821; GPE 2.

R InterPro; IPR00181; Chemokine ILG.

R InterPro; IPR00181; Chemokine ILG.

R InterPro; IPR00181; Chemokine ILG.

R InterPro; IPR00181; Canadomedin B.

R InterPro; IPR00181; Thrmbomoduln.

R PR00181; EGF CA, 14.

R PR0181; PR00001; EGF CA, 14.

R PR0181; PS00101; EGF CA, 14.

R PROSITE; PS001187; EGF CA, 14.

R EGF-Like comain.

R EGF-Like comain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1999 (TrEMBirel. 10, Created)
1-MAR-2003 (TrEMBirel. 25, Last sequence update)
01-MAR-2004 (TrEMBirel. 26, Last annotation update)
Hypothetical protein PFB0950w.
01-JUN-2001 (TIEMBLrel. 17, Created)
01-JUN-2001 (TIEMBLrel. 17, Last sequence update)
01-JUN-2004 (TIEMBLrel. 26, Last annotation update)
Ci-METAl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307 AA.
                                                                                                                                                                                                                                                                          Nakayama A., Satou Y., Satoh N.;
"Isolation and characterization of giona intestinalis metamorphosis.";
Dev. Genes Evol. 211:184-189(2001).
EMBL; AB041857; BAB40596.1; -.
HSSP; P00743; ICCF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=21347414; PubMed=11455433;
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=PFB0950w;
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                                                                                                                                                                                                                                                                                                                           MEDLINE-2225705; PubMed=12368864;
MEDLINE-22255705; PubMed=12368864;
Gardner M.J., Fall N., Fung E., White O., Berriman M., Hyman R.W.,
Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
Bisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M., S., Nene V., Shallom S.J., Subline B., Petreson J., Angluoli S.,
Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Pertea M., Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O., Fraesr C.M., Adams M.D., Venter J.C., Hoffman S.L., "Chromosome 2 sequence of the human malaria parasite Plasmodium falcibarum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94303173; PubMed=8030224;
Ayres M.D., Howard S.C., Kurlo J., Lopez-Ferber M., Possee R.D.;
"The complete DNA sequence of Autographa californica nuclear
polyhedrosis virus."
Virology 202:586-605(1994).
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
Hypothetical 34, 4 kDa protein in LEF3-IAP2 intergenic region.
Autographa californica nuclear polyhedrosis virus (AcMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
NCBI_TaxID=46015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

47.0%; Score 54.5; DB 2; Length 307;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 9; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  falciparum.";
Nature 419:498-511(2002).
Nature 419:498-511(2002).
EMBL; AE001428; AAC71979.2; -.
PIR, FAE0012. E71602.
INEAPTO: IPRO01368; TWPR.c6.
PROSITE; PS00652; TWFR.NGFR.1; UNKNOWN.1.
Hypothetical protein.
SEQUENCE 307 AA; 35537 MW; B95A3DB354D4BE71 CRC64;
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Hypothetical protein.
SEQUENCE 290 AA; 34408 MW; CA78BA9C8B5AB997 CRC64;
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                                                                                                                                                                                                            Science 282:1126-1132(1998).
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DB 1; Length 290;

46.6%; Score 54;

Gaps

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Name=T0187.8;
Caenorhabditis elegans.
Bukaryota; Metasoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
Chesi M., Brents L.A., Ely S.A., Bais C., Mesri E.A., Robbiani D., Kuehl W.M., Bergsagel P.L.; Extended (FEB-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AF238374; AAP97749.1; -- GO, GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                            / Match 46.1%; Score 53.5; DB 2; Length 174; Local Similarity 47.1%; Pred. No. 15; as 8; Conservative 2; Mismatches 4; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 53; DB 2; Length 164;
Pred. No. 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sims M.A.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; 256499; CAA91301.1; -.
PIR; T24272; T24272.
HSSP; P10968; 2CWG.
                                                                                                                                         174 AA; 17810 MW; BC9917E34470B9EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16499 MW; C002D48D36C9FCED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein T01B7.8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WormPep, 70187.6; CE03592.
InterPro; IPR001450; 4Fe4S ferredoxin.
InterPro; IPR006081; Defensin_alpha.
InterPro; IPR006209; EGF like.
InterPro; IPR001007; VWF_C.
InterPro; IPR001007; VWF_C.
PROSITE; PS001269; DEFENSIN; UNKNOWN_1.
PROSITE; PS001269; DEFENSIN; UNKNOWN_1.
PROSITE; PS01269; VWFC_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                     164 AA.
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STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GFCRCICTRGFCRCICTR 18
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                                                                                                                                                                                                                                                                                                   75 GLCVCVCV---CVCVCT 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Query Match
Best Local Similarity 50.v.,
Best and 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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SEQUENCE 164 AA; 1
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                                                                                                        Receptor.
NON TER
SEQUENCE
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Q95QY1;
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ID 09
AC 09
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          STXRRES
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                             Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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0
                                                                                                                                                                                                                                                                                                                                           Neurospora crassa.
Bukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.6%; Score 54; DB 2; Length 991; 56.2%; Pred. No. 59; tive 0; Mismatches 7; Indels
                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103024 MW; C51719B9F4D54A8E CRC64;
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-0UN-2003 (TrEMBLrel. 24, Last annotation update)
Mutant fibroblast growth factor receptor 3 (Fragment).
                                                                                                                                                                                                                                         01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                       991 AA
                           2; Mismatches
                                                                                         218 FARCFCTNTMQCFCPRQGYKCECICRR 244
                                                                2 FCRCICT-----RGF-CRCICTR 18
          Pred. No.
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                                                                                                                                                                                                       PRT;
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EMBL, AARXOL000029; EAA35288.1; -.
INTERFOR, IPRO06209; EGF_like.
PROSITE; PS00022; EGF_1.1.
PROSITE; PS01186; EGF_2; 1.
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      40.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GFCRCICTRGFCRCIC 16
        Best Local Similarity 40.79
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 56.2<sup>3</sup>
Matches 9; Conservative
                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                       Predicted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=5141;
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                                                                                                                                                                RESULT 13
Q7SEQ2
ID Q7SEQ2;
AC Q7SEQ2;
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Gaps

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RESULT 14 Q9NRB6

Caenorhabditis elegans. Eukaryothabditis elegans. Eukaryotdae, Metazoa, Nematoda, Chromadorea, Rhabditidae, Rhabditodae, Rhabditidae, Peloderinae, Caenorhabditis. NCBI_TaxID=6239; Wilson R.; "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998). STRAIN=Bristol N2,
STRAIN=Bristol N2,
Naterston R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; U55854; AAK68161.1; -.
HSSP; 109585; 1W7.
HSSP; 109585; 1W7.
HSSP; 109585; 1W7.
InterPro; 1PR001450; 4Fe4S_ferredoxin.
InterPro; 1PR006081; Defensin_alpha.
InterPro; 1PR006209; EGF_like.
InterPro; 1PR006209; EGF_like.
RINESPRO; 1PR006209; EGF_like.
RINESPRO; 1PR006209; EGF_like.
RINESPRO; 1PR006209; EGF_Like. Query Match
Best Local Similarity 50.0%; Pred. No. 19;
Matches 9; Conservative 0; Mismatches 9; Indels SEQUENCE FROM N.A.
STRANIE-Bristol N.Y.
Anderson K., Chissos S.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases. Nhan M.; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases. 017641, 01-NOV-1996 (TrEMBLrel. 01, Created) 01-OCT-2001 (TrEMBLrel. 18, Last sequence update) Hypothetical protein C04G6.7. ORFNames=C04G6.7; PRT; 197 AA. SEQUENCE FROM N.A. STRAIN-Bristol N2; MEDLINE=99069613; PubMed=9851916; 1 GFCRCICTRGFCRCICTR 18 81 GCGCCCCRPKCCCCCRR 98 PRELIMINARY; RESULT 18 Q17641 ID Q17641 ò ô 0; Gaps Caenorhabdītis —legans. Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdītida; Rhabdītoidea; Rhabdītidae; Peloderinae; Caenorhabdītis. NCBI_TaxID=6239; "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998). Query Match
Best Local Similarity 50.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 9; Indels MOSTE; F10969; IAN, WormPep (2006). CE27649. InterPro; IPR001450; 4F48_ferredoxin. InterPro; IPR001450; 4F48_ferredoxin. InterPro; IPR006209, EGF like... InterPro; IPR001007; VWF_C... InterPro; IPR001007; VWF_C... PROSITE; PS00129; 4F848_FERREDOXIN; UNKNOWN_I. PROSITE; PS00022; EGF 1; UNKNOWN_I. PROSITE; PS01208; VWFC_I; UNKNOWN_I. PROSITE; PS01208; VWFC_I; UNKNOWN_I. PROSITE; PS01208; VWFC_I; UNKNOWN_I. SEQUENCE 166 AA; 16971 MW; 9D9D130351BB50F1 CRC64; SEQUENCE FROM N.A. STRAIN=Bristol N2; Anderson K., Chissos S.; Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases. SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Waterston R.;
Submitted (MAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, U55854; AAK68158.1; -. Q18238 PRELIMINARY; PRT; 188 AA. Q18238.
Q18238.
01.NOV-1996 (TrEMBLrel. 01, Created)
01.NOV-1996 (TrEMBLrel. 02, Last sequence update)
Hyporhetical protein C27A2.5.
ORFNames=C27A2.5; SEQUENCE FROM N.A. STRAIN=Bristol N2; MEDLINE=99069613; PubMed=9851916; SEQUENCE FROM N.A. STRAIN=Bristol N2; MEDLINE=99069613; PubMed=9851916; Wilson R.; 81 ĠĠĠĠĊĊĊĸPŖĊĊĊĊĸŔ 98 1 GFCRCICTRGFCRCICTR 18

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Gaps ; No ESQUENCE FROM N.A.

SEQUENCE FROM N.A.

SITAIN=Bristol N2;

Waterston R.;

Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; US8760; AAX31463.1; -..

EMBL; US8760; AAX31463.1; -..

EMBL; US8760; AAX31463.1; -..

R PIN; TISE31; TISE31.

R PIN; TISE31; TISE31.

R MOVED CO:0005576; C:extracellular; IEA.

R GO: GO:0005576; Defense response; IEA.

R InterPro; IPR001409; 4Fe45 ferredoxin.

R InterPro; IPR001009; WWF C.

R PROSITE; PS001209; WFF245 FERREDOXIN; UNKNOWN_1.

R PROSITE; PS001209; WFF21; UNKNOWN_1.

R PROSITE; PS001209; WFF21; UNKNOWN_1.

R PROSITE; PS001209; WFF21; UNKNOWN_1. STRAIN-Bristol N2;

PDT TELEFORM OF THE STANK SOLUTION OF THE ST

"Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).

[2] SEQUENCE FROM N.A.

Wilson R.;

PAC DDT TABLE REPART RE

RESULT 17 Q18238

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(TrEMBLrel. 27,
                               PRELIMINARY;
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01-APR-2004 (
01-APR-2004 (
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BAD13491;
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YOSHIOKA S., Taniguchi F., Miura K., Inoue T., Yamano T., Fukuzawa H.

"A Novel Myb Transcription Factor LCR1 Regulates the CO2-Responsive
Gene Cahl Encoding A Periplasmic Carbonic Anhydrase in Chlamydomonas
reinhardtii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydomonas reinhardtii.
Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonas.
NCBI_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Asamizu E., Miura K., Kucho K., Inoue Y., Fukuzawa H., Ohyama K., Nakamura Y., Tabata S.; "Generation of expressed sequence tags from low-CO2 and high-CO2 adapted cells of Chimanydemonas reinhardtii.";
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0
                                                                                                                                       Score 53, DB 2; Length 197;
Pred. No. 20;
0; Mismatches 9; Indels
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45.7%; Score 53; DB 2; Length 602;
Best Local Similarity 75.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 3; Indels
PROSITE; PS00269; DEFENSIN; UNKNOWN 1.
PROSITE; PS01028; EGF 1; UNKNOWN 1.
PROSITE; PS01208; WPFC_1; UNKNOWN 1.
Hypothetical protein.
SEQUENCE 197 AA; 20596 MW; FB5F9457BFB9BBAD CRC64;
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Low-CO2 inducible Myb transcription factor LCR1.
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Les 9; Conservative
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SEQUENCE FROM N.A.
PubMed=14555782;
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SEQUENCE 602 1
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Matches 9
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Yoshioka S., Taniguchi F., Miura K., Inoue T., Yamano T., Fukuzawa H.;
Yoshioka S., Taniguchi F., Miura K., Inoue T., Yamano T., Fukuzawa H.;
A Novel Myb Transcription Factor LCR1 Regulates the CO2-Responsive
Gene Cahl Encoding A Periplasmic Carbonic Anhydrase in Chlamydomonas
reinhardtii.";
                                                                                                                                                                                                                                                                                                                                                                                       L42.

Kucho K., Yoshioka S., Taniguchi F., Ohyama K., Fukuzawa H.;

Kucho K., Yoshioka S., Taniguchi F., Ohyama K., Fukuzawa H.;

"Cas-acting elements and DNA-binding proteins involved in CO2-
"Cas-acting elements and DNA-binding proteins involved in CO2-
responsive transcriptional activation of Cahi encoding a periplasmic
carbonic anhydrase in Chlamydomonas reinhardtii.";

Plant Physiol. 133:783-793(2003).

EMBL; AB168089; BAD13491.1;

SEQUENCE 602 AA; 62736 MW; 3DD94253D5A792D0 CRC64;
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                                                                                             Chlamydomonas reinhardtii.
Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlamydomonas reinhardtii.
Ukaryota, Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaeae; Chlamydomonas.
NCBI_TaxID=3055;
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DNA Res. 7:305-307(2000).
EMBL: AB168090; BAD13492.1, -
SEQUENCE 602 AA, 62736 MW; 3DD942S3D5A792D0 CRC64;
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01-APR-2004 (TrEMBLrel. 27, Last sequence update) 01-APR-2004 (TrEMBLrel. 27, Last annotation update) Low-CO2 inducible Myb transcription factor LCR1.
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01-APR-2004 (TrEMBLrel. 27, Last seq
01-APR-2004 (TrEMBLrel. 27, Last ann
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Best Local Similarity
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Query Match Q75N87 RESULT 25
BAD16739
ID BAD16
AC BAD16
DT 26-AP Best Loc Matches RESULT 24 Q75N87 ò d SO RET ð ö NO SEQUENCE FROM N.A.

Uyeda T., Takahashi T., Eto S., Sato T., Xu G., Toki T., Yonesaka S.,

Uyeda T., Takahashi T., Eto S., Sato T., Xu G., Toki T., Yonesaka S.,

Lo E.;

Submitted (APR-2004) to the EWBL/GenBank/DDBJ databases.

-!- SIDMILARITY: Contains 2 EGF-like domains.

SERL, ABIT7802; BAD16738-1; -
SERL, ABIT7802; BAD16738-1; -
SERL, ABIT7802; BAD16738-1; -
SERL, ABIT7802; BAD16738-1; -
InterPro; IPR001439; EGF_Ca.

SINTER-Pro; IPR001439; EGF_IL.

SERL, SEQUENCE FROM N.A. Uyeda T., Takahashi T., Eto S., Sato T., Xu G., Toki T., Yonesaka S., Ito E., Gaps Homo sapiens (Human). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. NCBI_TaxID=9606; ; 0 Query Match

Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 9; Conservative 1; Mismatches 5; Indels RESULT 23
BAD16738

AC BAD16738

DT 26-APR-2004 (TrEMBLrel. 27, Created)
DT 26-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT 26-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT 26-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibrillin 1.
GN FBNI.
GN FBNI.
GN HOMO sapiens (Human).
OC Mumanalia; Metazoa; Chordata; Craniata; Vertebrata; But OC Mumanalia; Butheria; Primates; Catarrhini; Hominidae; HOON NCBI TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Uyeda T., Takahashi T., Eto S., Sato T., Xu G., Toki T.R.
RA Uyeda T., Takahashi T., Eto S., Sato T., Xu G., Toki T.R.
RA Uyeda T., Takahashi T., Eto S., Sato T., Xu G., Toki T.R.
RA Uyeda T., Takahashi T., Eto S., Sato T., Xu G., Toki T.R. Q75N88; 05-UUL-2004 (TrEMBLrel. 27, Created) 05-UUL-2004 (TrEMBLrel. 27, Last sequence update) 05-UUL-2004 (TrEMBLrel. 27, Last annotation update) Fibrillin 1. 464 RCIPTPGSCRCECNK 478 4 RCICTRGFCRCICTR 18 471 CTRCQCRCICCR 482 PRELIMINARY; Q75N88 RESULT 22 5N88 SOW WHEN THE PROPERTY OF THE P g 8

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Momo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"3 Novel mutations of Fibrillin-1 and 10 single nucleotide polymorphisms of Fibrillin-3 in Marfan syndrome patients."; submitted (APR-2004) to the BNBL/GenBank/DDBJ databases. BRBL, AB177802, BAL16738-1.; -. SEQUENCE 1365 AA; 147448 MW; ED83FB79C1B2BD48 CRC64;
                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 9; Conservative 1; Mismatches 5; Indels
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Fibrillin 1.
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BAD16739;
26-APR-2004 (TrEMBLrel. 27, Created)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Wistar; TISSUE-Hippocampus;
Andriamampandry C., Taleb O., Viry S., Muller C., Humbert J.P.,
Goballe S., Aunis D., Maitre M.;
"Cloning and characterization of a rat brain receptor that binds the
endogenous neuromodulator gamma-hydroxybutyrate.";
PASEB J. 6:-0(2004).
EMBL; 9445593; AR24022.1; -
GO, GO:0004872; F:receptor activity; IEA.
InterPro; IPR001209; Ribosomal S14.
InterPro; IPR001951; Tetraspanin.
InterPro; IPR001951; Tetraspanin.
PF00335; Tetraspanin; I.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                               Length 273;
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                                                                                                                                                                                                                                                               3; Indels
                                                                                            Aphasizhev R., Aphasizheva I., Simpson L.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF411047; AALOS568 1; - CAS21A819A9E564 CRC64;
SEQUENCE 273 AA; 31149 MW; 4C0321A819A9E564 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          512 AA; 56146 MW; 44DD12B937C40D60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-WAR-2004 (TrEMBLrel. 27, Created)
02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                               45.3%; Score 52.5; DB 2; 50.0%; Pred. No. 30; iive 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               512 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00259; TMFOÜR.
PROSITE; PS00527; RIBOSOMAL_S14; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.3%; Score 52.5; D
50.0%; Pred. No. 52;
tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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STRAIN=Wistar; TISSUE=Hippocampus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gamma-hydroxybutyrate receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gamma-hydroxybutyrate receptor.
                                                                                                                                                                                                                                                                                                                                          253 CVCVCV---CVCVCTR 265
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                                                                                                                                                                                                                                      Best Local Similarity 50.0 Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 50.0.
Best Local Similarity
6, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
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  lizard Leishmania.
NCBI_TaxID=5689;
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                                                                        SEQUENCE FROM N.A
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AAR24072;
02-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor.
SEQUENCE
                                                                                                                                                                                                               Query Match
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110 AAR2

AA AAC2

DT 02-W

DT 02-W

DT 02-W

DT 02-W

OC BACE

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OC MAN

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                                                                                                                                                                                                          SEQUENCE FROM N.A.
Uyeda T., Takahashi T., Eto S., Sato T., Xu G., Toki T., Yonesaka S.,
Ito E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ENSANGPO0000023822 (Fragment).
Name=ENSANGG0000020032;
Anophales gambiae str. PEST.
Buckaryota, Metazoa, Arthropoda, Hexapoda; Insecta, Pterygota;
Neoptera, Endopterygota, Diptera; Nematocera; Culicoidea; Anophales.
NCBI_TAXID=180454;
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01-DEC-2001 (TrEMBLrel. 24, Last sequence update)
01-DGC-2003 (TrEMBLrel. 24, Last annotation update)
28 kDa guide RNA binding protein.
1eishmania tarentolae (Sauroleishmania tarentolae).
Mitochondarion.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania;
                                                                                                                Eukaryota, Metazoa, Chordata; Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anopheles Genome Sequencing Consortium,
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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1
                                                                                                                                                                                                                                                                            "3 Novel mutations of Fibrillin-1 and 10 single nucleotide polymorphisms of Fibrillin-3 in Marfan syndrome patients."; Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases. EMBL; AB177803; BAD16739.1; -. SEQUENCE 2871 AA; 312219 MW; C3D044AB0321E082 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.3%; Score 52.5; DB 2; Length 129; 50.0%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                          45.7%; Score 53; DB 2; Length 2871; 60.0%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 129
129 AA; 13897 MW; C3D9F1EB9EF65B74 CRC64;
26-APR-2004 (TrEMBLrel. 27, Last sequence update)
56-APR-2004 (TrEMBLrel. 27, Last annocation update)
Fibrillin 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preliminary data.
; AAAB01008964; EAA43873.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    464 RCIPTPGSCRCECNK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 CRCICTRGFCRCICTR 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 RCICTRGFCRCICTR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 60.0 es 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 50.0
Matches 8; Conservative
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                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=PEST;
                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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NON_TER
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PRT; 1823 AA
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InterPro, IPR00152; Asx hydroxyl_S.
InterPro, IPR00742; EGF_2.
InterPro, IPR006209; EGF_like.
InterPro; IPR001410; Hyalin.
InterPro; IPR001791; Laminin_G.
                                                                                                                                                                                                                                                    PRT;
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                   Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
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Best Local Similarity 52.99
Matches 9; Conservative
                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                       S CICTRGFCRCI 15
                                                                                                                             |:| |:||;
44 CVCVLGWCRCV 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7227;
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Q7PRP5
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Andriamampandry C., Taleb O., Viry S., Muller C., Humbert J.P., Gobaille S., Aunis D., Maitre M.; "Cloning and characterization of a rat brain receptor that binds the endogenous neuromodulator gamma-hydroxybutyrate."; EASEB J. 0:0-0(2004).
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AgCP1494 (Fragment).
Name=agCG47401; ORFNames=ENSANGG0000012913;
Anopheles gambiae Str. PET.
Bubaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yranulovirus).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
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MEDLINE=9943-230; PubMed=10502508;

MEDLINE=9943-230; PubMed=10502508;

HayAkawa T., Ko R., Okano K., Seong S.I., Goto C., Maeda S.;

"Sequence analysis of the Xestia c-nigrum granulovirus genome.";

"Sequence analysis of the Xestia c-nigrum granulovirus genome.";

"Indexional Second Secon
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Anopheles Genome Sequencing Consortium;
Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL; AAAB01008859; EAA07639.1; -.
NON TER 1
SEQÜENCE 146 AA; 16746 MW; 7D32B8AABE776F98 CRC64;
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                                                                                                                                                                                             DB 2; Length 512;
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                                                                                                                                                                                                                                    5; Indels
                                                                                                                                                 512 AA; 56146 MW; 44DD12B937C40D60 CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                           66 AA.
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Local Similarity 50.0%; Pred. No. 52;
tes 8; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                                                                                                                                      386 ČVČVČVŘ-VČLČLČVŘ 400
                                                                                                                                                                                                                                                                              3 CRCICTRGFCRCICTR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9FYQ3;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2002 (TrEMBLrel. 22,
ORF143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=ORF143;
                                                                                                                                                                                             Query Match
Best Local S:
Matches 8
                                                                                                                                                       SEQUENCE
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Matches
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Berkeley; Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Chapteton M., Brokstein P., Hong L., Agbayani A., Carlson J., Exise B., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise B., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S. Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anopheles Genome Sequencing Consortium;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAVITON: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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01-CCT-2002 (TrEMBLrel. 22, Last sequence update)
01-CCT-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Evaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Ephydroidea; Endoptertygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.8%; Score 52; DB 2; Length 161; 52.9%; Pred. No. 22;
Score 52; DB 2; Length 146;
Pred. No. 20;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases EMBL; AY113346; AAM29351.1; -. FlyBase; FBGN0063249; BcDNA:GH14618. SEQUENCE 161 AA; 17659 MW; EB41C9D94274EE94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
1-WAR-2004 (TrEMBLrel. 26, Last annotation update)
ENSANGPO000019046 (Fragment).
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Pfam, PF00228; Bowman-Birk_leg; 2.
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PDB; 1DF9; X-ray; C=1-72.
PDB; 1G91; X-ray; I=10-31.
PDB; 1SBW; X-ray; I=8-42.
PDB; 1SWF; X-ray; I=10-31.
InterPro; IPR000877; Prot_inl
                                                                                                                                                                                                                                                                                                                                                                          3 CRCICTRGFCRCICT 17
                                                                                                                                                                                                                                                                                                                                                                                                        CPCCCQCGECCCCT 57
                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 53.3%
....hos 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI TaxID=3916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBB_PHAAU
P01062;
                                                                                                                                                                                                                                                                                                                                                                                                          43
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                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

TISSUE=Liver;
Zhang C., Yu Y., Zhang S., Ouyang S., Luo L., Wei H., Zhou G.,
Zhang Y., Liu M., He F.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.

EMBL, AF111848; AAF16687.1;
SEQUENCE : 190 AA; 21480 MW; 4B8104A29AA33844 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.4%; Score 51.5; DB 2; Length 190; 47.1%; Pred. No. 30; tive 2; Mismatches 4; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                         Length 1823;
                                                                                                                                                                                                                                                                                                                                                                          Score 52; DB 2; Length 182
Pred. No. 1.88+02;
                                                                                                                                                                                                                                                                                                                                                            200582 MW; 5740C4C700804379 CRC64;
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Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                      ProDom; PD002153; Pentaxin; 1.
PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PS00022; EGF_1; UNKNOWN_5.
PROSITE; PS01186; EGF_2; 4.
PROSITE; PS50026; EGF_2; 3; 5.
PROSITE; PS50825; HYR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
InterPro; IPR001759; Pentaxin.
InterPro; IPR001211; PhospholipaseA2.
InterPro; IPR001211; PhospholipaseA2.
InterPro; IPR0012035; VWF_A.
Pfam; PF012494; HYR; 2.
Pfam; PF00184; PR01494; Pentaxin; 1.
Pfam; PF00084; Sushi; 8.
Pfam; PF00084; Sushi; 8.
Pfam; PF00085; PRNTAXIN.
PRINTS; PR00895; PRNTAXIN.
                                                                                                                                                                                                                 PROSITE; PS01186; EGF_2; 4.
PROSITE; PS50026; EGF_3; 5.
PROSITE; PS50025; LAM G DOMAIN; 1.
PROSITE; PS00118; PA2 HIS; UNKNOWN I.
PROSITE; PS50923; SUSHI; 8.
PROSITE; PS50934; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last seq
105-JUL-2004 (TrEMBLrel. 27, Last ann
105-JUL-2004 (TrEMBLrel. 27, Last ann
08-RNames=HDC07368;
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Q9U123;
Q9U123;
01-MAY-2000 (TrEMBLrel. 13, C)
01-MAY-2000 (TrEMBLrel. 13, L6)
01-OCT-2002 (TrEMBLrel. 22, L6
PRO0529.
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                                                                                                                                                                                                                                                                                                                                                                                         44.8%;
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263 CSCLTTSGHYRCIC 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 CRCICTRGFCRCIC 16
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Best Local Similarity 57.1%
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                                                                                                                                                                                                                                                                                                                                             1823 182
1823 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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NON TER
SEQUENCE
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09UI23
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Q61G37
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MEDINE-95596014; PubMed=7798176;

X. RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 10-31, AND REVISIONS.

MEDINE-95596014; PubMed=7798176;

I.Y., Huang Q., Zhang S., Liu S.,

I.Y., Huang Q., Zhang S., Liu S.,

I.Y., Tang Y.;

Istudies on an artificial trypsin inhibitor peptide derived from the activated and analysis of its complex with trypsin.";

I.Y., Tang Y.;

I.Y., T
                                                                                                                                                                                                                                                                        MEDLINE-82249808; PubMed-6125033;
Zhang Y., Luo S., Tan F., Qi Z., Xu L., Zhang A.;
"Complete amino acid sequence of mung bean trypsin inhibitor.";
Sci. Sin., Ser. B, Chem. Biol. Agric. Med. Earth Sci. 25:268-277(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bowman-Birk type trypsin inhibitor.
Phaseolus aureus (Mung bean) (Vigna radiata).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Belongs to the Bowman-Birk serine protease inhibitor
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Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bhydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 51; DB 2; Length 59;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Indels
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01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
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PRINTS; PRO0438; GFCYSKNOT.
ProDom; PD001629; PD_growth_factor; 1.
SMART; SM00141; PDGF; 1.
PROSITE; PS50278; PDGF 1; 1.
PROSITE; PS50278; PDGF 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                               3 CRCICTRGFCRCIC 16
                                                                                                                                                                                                                                                                                                                                                                                                                     59 CLCVCLVSVCLCVC 72
                                             PRELIMINARY;
                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10047;
                                                                                                                                                       NCBI_TaxID=9606;
                                              BAC87611
BAC87611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q91ZH6
Q91ZH6;
                        RESULT 38
BAC87611
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       091ZH6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUB-Thalamus, Thibashi T., Chiba Y., Fujimori K., Hiraoka S., Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S., Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M., A Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M., A Sugiyama T., Irie R., Orsuki T., Saro H., Wakamatsu A., Ishii S., Yamamoro J., Isono Y., Nawai-Hio K., Saito K., Nikuchi H., Kanda T., Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., A Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

R EMBL, AK12879; BAC87611.1; -

REMBL, AK12879; BAC87611.1; -

REMBL, AK12879; BAC87611.1; -

R InterPro; IPRO6209; EGF Like.

R REOSITE; PS01186; EGF 2; UNKNOWN 1.

R PROSITE; PS01186; EGF 2; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                            Gaps
Probom, PD002168; Bowman-Birk_leg; 1.

SMART; SM00269; BowB; 1.

SMART; SM00269; BowB; 1.

3D-structure; Direct protein sequencing; Serine protease inhibitor.

SITE 47 48 Reactive bond for trypsin.

DISULFID 12 66 By similarity.

DISULEID 13 28 By similarity.

DISULEID 16 62 By similarity.
                                                                                                                    By similarity.
By similarity.
By similarity.
By similarity.
Missing (in 2nd and 3rd isoinhibitor).
H -> D (in 1st isoinhibitor).
D -> K (in 3rd isoinhibitor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OGZOS2 PRELIMINARY; PRT; 201 AA.

06.20.2.;
05.JUL-2004 (TrEMBLrel. 27, Created)
05.JUL-2004 (TrEMBLrel. 27, Last sequence update)
05.JUL-2004 (TrEMBLrel. 27, Last annotation update)
05.JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypotherical protein FLJ45585.
Homo sepiens (Human).
Homo sepiens (Human).
Homo sepiens (Aberaca; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                 44.0%; Score 51; DB 1; Length 72; 57.9%; Pred. No. 15; 2; Indels ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                             7959 MW; 8359DE1A8E61E4F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 40 CKSCICTRSMPGKCRCLDT 58
                                                                                                                                                                                                                                                                                                                                                                                                   3 CR-CICTR---GFCRCICT 17
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| | : | | | | | 5
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Best Local Similarity 57.9
Matches 11, Conservative
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VARIANT
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Matches
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Q6ZQS2
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Kanebori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,
Kanebori K., Ishibashi T., Chiba Y., Fujimori T., Watanabe M.,
Sugiyama T., Irie R., Cishki T., Sato H., Wakamatsu A., Ishii S.,
Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
Yamamoto J., Isono Y., Kawai-Hio Y., Sekine M., Kikuchi H., Kanda K.,
Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
Suziki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
"NEDO human CDNA sequencing project.";
Submitted (JUL-2003) to the EMBL/Genbank/DDBJ databases.
EMBL; AK128797; BACG7611.1;
SEQUENCE 201 AA, 20938 MW; 3408FBEBITAAO500 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=vegfc;
Mariones unguiculatus (Mongolian jird) (Mongolian gerbil).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
                                                   02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
CDNA FLJ45585 fis, clone BRTHA3013882.
Endo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
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44.0%; Score 51; DB 2; Length 201;
Best Local Similarity 42.9%; Pred. No. 36;
Matches 6; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
vascular endothelial growth factor C (Fragment).
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201
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Gaps
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ENSANGPO0001010200 (Fragment).
Name=ENSANGG0000008031;
Anopheles gambiae str. PEST.
ENKAryota; Metazoa; Arthopoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NGT TAXID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Another Genome Sequencing Consortium,
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-- CAUTION: The Sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL, AAAB01009984; EAA14914.1; -.

NON_TER 336
SEQÜENCE 336 AA, 36383 MW; 0C28D220B6E129A8 CRC64;
                                                                                                                                                                          10;
                                                                                                         Query Match
Best Local Similarity 36.0%; Pred. No. 55;
Matches 9; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 44.0%; Score 51; DB 2; Length 336; Best Local Similarity 55.6%; Pred. No. 56; Matches 10; Conservative 1; Mismatches 3; Indels
Growth factor; Mitogen. Now TER _{\rm 1} _{\rm 1} SEQUENCE 326 AA; 36826 MW; D0B2772C77836914 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                           336 AA.
                                                                                                                                                                                                                                                                              246 COCVCKRTCPRNOPINPGKCTCECT 270
                                                                                                                                                                                                                         3 CRCICTR-----GFCRCICT 17
                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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SPT
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2;

Gaps

4

Search completed: October 26, 2004, 15:39:20 Job time : 131.5 secs

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RESULT 2
US-09-967-808-1
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US-09-309-487-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                            Sequence 1, Sequence 2, Sequence 3, Sequence 4, Sequence 5, Sequence 6, Sequence 7, Sequence 7, Sequence 8, Sequence 9, Sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1,
Sequence 9,
Sequence 9,
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3: /cgn2_6/ptodata1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata1/iaa/FQTUG_COMB.pep:*
6: /cgn2_6/ptodata1/iaa/PQTUG_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Sequence 1, Appli Sequence 20, App Sequence 20, Appl Sequence 20, Appl Sequence 27, Appl Sequence 121, Appl Sequence 65, Appl Sequence 69, Appl Sequence 12502, Appl Sequence 32502, Appl Sequence 55500, A Sequence 55500, A Sequence 5550, A Sequence 5550, A Sequence 5550, A Sequence 5550, A Sequence 5550, A Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 2550, A	Sequence 4, Appli
US-10-042-872-1 US-09-510-2383-286 US-09-967-988-20 US-09-967-988-20 US-10-141-645-45 US-10-141-645-45 US-10-141-645-65 US-10-141-645-69 US-10-141-645-69 US-10-141-645-69 US-09-270-767-767-755-20 US-09-270-767-755-20 US-10-141-645-12 US-09-270-767-755-20 US-10-141-645-12 US-10-141-645-12 US-10-141-645-12 US-10-141-645-12 US-10-141-645-12 US-08-899-811-4	US-09-042-105-4
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## ALIGNMENTS

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| Sequence 1. Application US/09309487 | Sequence 1. Application US/09309487 | Sequence 1. Application US/09309487 | Sequence 1. Applicant No. 633538 | Sequence 1. INPORMATION: APPLICANT: Selsted, Michael E. APPLICANT: Yuan, Jun APPLICANT: Yuan, Jun APPLICANT: Ouellette, Andre J. TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same | TITLE REFERENCE: PUC 3095 | SURRET PRILITY APPLICATION NUMBER: US/09/309,487 | CURRET FILING DATE: 1999-05-10 | NUMBER OF SEQ ID NOS: 31 | SEQ ID NO 1 | LENGTH: 18 | L
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Sequence 1, Application US/09967808

Patent No. 6514727

GENERAL INFORMATION:

APPLICANT: Tang, Yi-Quan

APPLICANT: Tang, Yi-Quan

APPLICANT: Ouellette, Andre J.

TITLE OF INVENTION: Anner J.

TITLE OF INVENTION: Anner J.

FILE REPRENCE: PUC 3095

CURRENT APPLICATION NUMBER: US/09/967,808

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: US/09/309,487

PRIOR PLIJNG DATE: 1999-05-10

NUMBER OF SEQ ID NOS: 31

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 18
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Pred. No. 8.6e-06;
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Best Local Similarity 83.3
Matches 15; Conservative
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SEQUENCE I, Application US/10141645
Patent No. 6713078
Farmal Information
APPLICANT: Robert Lehrer
APPLICANT: Alaw Maring
APPLICANT: Alawander Cole
APPLICANT: Teresa Hong
ITILE OF INVENTION: Retrocyclins - Antiviral
APPLICANT: Teresa Hong
ITILE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-001CIP
CURRENT FILING DATE: 2002-06-06
PRIOR PRICATION NUMBER: 60/284,855
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SEQ ID NOS: 125
LENGTH: 18
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LENGTH: 18
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APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-001C1P
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: US/0244,855
PRIOR APPLICATION NUMBER: Ussigned
PRIOR FILING DATE: 2002-04-18
PRIOR FILING DATE: 2002-04-18
PRIOR FILING DATE: 2002-04-18
SROFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: Inc.
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Patent No. 6713078
GENERAL INFORMATION
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
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Best Local Similarity 61.1%;
Matches 11; Conservative
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CRGANISM: Homo sapiens
US-10-141-645-1
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Best Local Similarity
                                                                                       US-10-141-645-1
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GENERAL INFORMATION:
APPLICANT: Selected, Michael E.
APPLICANT: Tang, Yi-Quan
APPLICANT: Tang, Yi-Quan
APPLICANT: Vann, Jun
APPLICANT: Vann, Jun
APPLICANT: Ovellette, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
FILE REFERENCE: P-UC 3095
CURRENT APPLICATION NUMBER: US/09/309,487
CURRENT FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 18
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APPLICANT: Yuan, Jun
APPLICANT: Yuan, Jun
APPLICANT: Yuan, Jun
APPLICANT: Oucllette, Andre J.
ITILE OF INVENTION: Same
FILE REFERENCE: P-UC 3095
CURRENT APPLICATION NUMBER: US/09/967,808
CURRENT APPLICATION NUMBER: US/09/309,487
PRIOR FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver: 2.0
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Pred. No. 8.6e-06;
1; Mismatches 2; Indels
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Best Local Similarity 87.5%; Pred. No. 2.5e-05;
Matches 14; Conservative 1; Mismatches 1
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; Sequence 9, Application US/09967808
; Patent No. 6514727
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Patent No. 6335318
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                                                                                    Query Match
Best Local Similarity 83.3%;
Matches 15; Conservative
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APPLICANT: Selsted, Michael E.

; TYPE: PRT
; ORGANISM: Macaca mulatta
US-09-967-808-1
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US-09-309-487-9
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US-09-309-487-9
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Query Match

78.6%; Score 88; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.00016;
Matches 12; Conservative 3; Mismatches 3; Indels
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GENERAL INFORMATION:
APPLICANT: ROBET Lehrer
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
TITLE OF INVENTION: Antimicrobial Peptides
TITLE OF INVENTION: Antimicrobial Peptides
CURRENT APPLICATION WINDER: US/10/141,645
CURRENT APPLICATION NUMBER: 00/284,855
PRIOR PILING DATE: 2001-04-18
PRIOR PILING DATE: 2001-04-18
PRIOR PILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: Unassigned
PRIOR APPLICATION NUMBER: Unassigned
SRIOR FILING DATE: 2001-04-18
SROID NO 6
SEQ ID NO 6
ILENGTH: 18
US-10-141-645-5

Sequence 5, Application US/10141645

Sequence 5, Application US/10141645

Sequence 5, Application US/10141645

GENERAL INFORMATION:

APPLICANT: Robert Lehrer

APPLICANT: Alexander Cole

APPLICANT: Teresa Hong

TITLE OF INVENTION: Retrocyclins - Antiviral and

TITLE OF INVENTION: Antimicrobial Peptides

TITLE OF INVENTION: Antimicrobial Peptides

FILE REPERRENCE: UCLA-001CIP

CURRENT APPLICATION NUMBER: US/10/141,645

CURRENT FILING DATE: 2001-04-18

PRIOR PILING DATE: 2001-04-18

PRIOR PLING DATE: 2002-04-18

NUMBER OF SEQ ID NOS: 125

SOOFTWARE: FASISEC for Windows Version 4.0
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ORGANISM: Artificial Sequence
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LENGTH: 18
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Sequence 4, Application US/10141645

Sequence 18 Application US/10141645

Sequence 18 Application US/10141645

SERENTAL INFORMATION:
APPLICANT: Alexander Cole
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
ITILE OF INVENTION: Retrocyclins - Antiviral and
FILE REPRENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645

CURRENT PILING DATE: 2002-05-06

CREOR FILING DATE: 2001-04-18

PRIOR FILING DATE: 2001-04-18

PRIOR FILING DATE: 2002-04-18

PRIOR FILING DATE: 2002-04-18

SEOFWARE: FastSEQ for Windows Version 4.0

SSOFWARE: FastSEQ for Windows Version 4.0
     OS-LOTALINGS
Dequence 3, Application US/10141645
Patent No. 6713078
GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alan Waring
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REPERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: 05/264,855
PRIOR APPLICATION NUMBER: 60/284,855
PRIOR FILING DATE: 2002-05-06
PRIOR FILING DATE: 2002-06-18
PRIOR FILING DATE: 2002-06-18
PRIOR PRILING DATE: 2002-06-18
PRIOR FILING DATE: 2002-06-18
SEQ ID NOS: 125
SEQ ID NOS: 125
LUNGTH: 18
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; OTHER INFORMATION: synthetic variant
US-10-141-645-3
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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1 GVCRCLCRRGVCRCLCRR 18

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1 GVCRCLCRRGVCRCLCRR 18

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Score 77; DB 4; Length 18; Pred. No. 0.0031; 4; Mismatches 4; Indels
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                                                                                              GENERAL NO. 0.12070)

APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alan waring
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT APPLICATION NUMBER: 00/284,855
PRIOR APPLICATION NUMBER: 00/284,855
PRIOR FILING DATE: 2001-04-18
FRIOR FILING DATE: 2002-05-06
PRIOR FILING DATE: 2002-06-18
FRIOR PRILING DATE: 2002-06-18
FRIOR FILING DATE: 2002-06-18
FRIOR APPLICATION NUMBER: Unassigned
FRIOR FILING DATE: 2002-06-18
FRIOR FILING DATE: 2002-06-18
FRIOR FILING DATE: 2002-06-18
FRIOR APPLICATION NUMBER: Unassigned
FRIOR 
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APPLICANT: Alan Waring
APPLICANT: Alan Alan Waring
APPLICANT: Teresa Horiographic Applicant: Teresa Horiographic Applicant: Teresa Horiographic Applicant Cole Applicant Cole Application Correct Application VICLA-OulCip Correct Application VICLA-OulCip Correct File Reference: VICLA-OulCip Correct File Reference: 2002-05-06
CURRENT FILING DATE: 2002-05-06
PRIOR PRICATION NUMBER: 60/284,855
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SSCPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: synthetic variant US-10-141-645-8
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US-10-141-645-8; Sequence 8, Application US/10141645; Patent No. 6713078
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US-10-141-645-9
Sequence 9, Application US/10141645
Patent No. 6713078
GENERAL INFORMATION
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ORGANISM: Artificial Sequence
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Best Local Similarity 55.6%;
Matches 10; Conservative
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ORGANISM: Artificial Sequence
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Matches 10; Conserva
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Pred. No. 0.00036;
3; Indels
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                                                                                                                                                                                                        APPLICANT: Alam Waring
APPLICANT: Alam Waring
APPLICANT: Alamader Cole
APPLICANT: Teresa Hong
ITILE OF INVENTION: Retrocyclins - Antiviral and
ITILE OF INVENTION: Antimicrobial Peptides
FILE REPERENCE: UCLA-OOLCIP
CURRENT APPLICATION NUMBER: US/284,855
PRIOR APPLICATION NUMBER: 00/284,855
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: Fastes@ for Windows Version 4.0
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Fatent No. 6696238
GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: Reid, Ted W.
TILLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: 05/21,632
PRIOR PILING DATE: 2001-07-29
PRIOR PILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-01-17
PRIOR PILING DATE: 2001-01-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PARENT NOS: 96
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; OTHER INFORMATION: synthetic variant
US-10-141-645-7
                                                          Sequence 7, Application US/10141645
Patent No. 6713078
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 61.1%;
Matches 11; Conservative
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; ORGANISM: Macaca mulatta
US-09-917-340-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
US-09-917-340-53
                                   JS-10-141-645-7
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Score 62; DB 4; Length 141;
Pred. No. 0.91;
1; Mismatches 1; Indels
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JAPPLICANT: Robert Lehrer
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-001CIP
CURRENT FILING DATE: 2002-05-06
PRIOR PRIOR PELICATION NUMBER: 60/284,855
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2002-04-18
PRIOR FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: FASTESCO for Windows Version 4.0
SEQ ID NO 72
LENGTH: 141
TYPE: PRT
TYPE: PRT
APPLICANT: Alan Waring
APPLICANT: Teres Hong
TERES Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Actimicrobial Peptides
FILE REPERENCE: UCLA-001CIP
CURRENT PILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 06/284,855
PRIOR APPLICATION NUMBER: 06/284,855
PRIOR APPLICATION NUMBER: USP
PRIOR APPLICATION NUMBER: USP
PRIOR PILING DATE: 2001-04-18
PRIOR PILING DATE: 2001-04-18
PRIOR PILING DATE: 2002-04-18
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COCATION: 113
COTHER INFORMATION: Xaa = Any Amino Acid
US-10-141-645-72
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Patent No. 6713078
GENERAL INFORMATION:
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Best Local Similarity 83.3%;
Matches 10; Conservative
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Best Local Similarity 78.6
Matches 11; Conservative
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69 RCICRRGVCRLL 80
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CRGANISM: Orangutan
US-10-141-645-68
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US-10-141-645-72
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US-10-141-645-66
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Sequence 22, Application US/09309487

Patent No. 6335318

GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Tang, Yi-Quan
APPLICANT: Tang, Yi-Quan
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
FILE REPERENCE: P-UC 3095
CURRENT APPLICATION NUMBER: US/09/309,487
CURRENT FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
LENGTH: 92
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| Sequence 22, Application US/09967808
| Patent No. E514727
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Tang, Yi-Quan |
| APPLICANT: Tang, Yi-Quan |
| APPLICANT: Van, Jun |
| APPLICANT: Outlette, Andre J. |
| TITLE OF INVENTION: Anne J. |
| TITLE OF INVENTION: Anne J. |
| TITLE OF INVENTION: Same |
| TITLE OF INVENTION NUMBER: US/09/967,808 |
| CURRENT PILING DATE: 1999-05-10 |
| NUMBER OF SEQ ID NOS: 31 |
| SEQ ID NO 22 |
| LENGTH: 92 |
| LENGTH: 93 |
| LENGTH: 94 |
| LENGTH: 94 |
| LENGTH: 95 
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Pred. No. 0.64;
1; Mismatches 2; Indels
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Pred. No. 0.64;
1; Mismatches
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Patent No. 6713078
GENERAL INFORMATION:
APPLICANT: Robert Lehrer
                         55.4%;
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Best Local Similarity 78.6%;
Matches 11; Conservative
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Best Local Similarity 78.6
Matches 11; Conservative
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, OKGANISM: Macaca mulatta
US-09-967-808-22
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ORGANISM: Macaca mulatta
US-09-309-487-22
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US-09-309-487-22
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US-09-967-808-22
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; TYPE: PRT
; ORGANISM: Macaca mulatta
US-09-309-487-16
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US-09-967-808-16
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                                                                                                                                     SEQ ID NO 16
LENGTH: 76
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LENGTH: 76
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Pred. No. 1.2;
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Pred. No. 1.2;
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  APPLICANT: Kudet Lucine.
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-001C1P
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 06/284,855
PRIOR APPLICATION NUMBER: 06/284,855
PRIOR APPLICATION NUMBER: Unassigned
PRIOR PILING DATE: 2002-04-18
PRIOR FILING DATE: 2002-04-18
PRIOR FILING DATE: 2002-04-18
SROFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 67, Application US/10141645
Patent No. 6713078
GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alaxander Cole
APPLICANT: Alexander Cole
APPLICANTON ANTINGICADIA PEDIA
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT APPLICATION NUMBER: 60/284,855
PRIOR FILING DATE: 2001-04-18
FRIOR FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SEOTUMARE: FASTSEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
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Patent No. 6335318
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Conservative
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Best Local Similarity 83.3
Matches 10; Conservative
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68 RCICRRGVCRFL 79
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APPLICANT: Robert Lehrer
                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Orangutan
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 10; Conserv
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US-10-141-645-67
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APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
FILE REPERBNCE: P-UC 3095
CURRENT APPLICATION NUMBER: US/09/309,487
CURRENT FILMG DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tang, Xi-Quan
APPLICANT: Yuan, Jun
APPLICANT: Yuan, Jun
APPLICANT: Yuan, Jun
APPLICANT: Vuan, Jun
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using
TITLE OF INVENTION: Same
FILE REPERENCE: P-UC 3095
CURRENT APPLICATION NUMBER: US/09/967,808
CURRENT FILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: US/09/309,487
PRIOR APPLICATION NUMBER: US/09/309,487
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                 Score 60; DB 3; Length 76; Pred. No. 0.94;
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                                                                                                                                                                                                                                                                                        1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence 16, Application US/09967808; Patent No. 6514727
Patent No. Patent No. 6514727
SENERAL INFORMATION: APPLICANT: Selsted, Michael E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.6%;
83.3%;
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Best Local Similarity 83.3
Watches 10, Conservative
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Matches 10; Conservative
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ORGANISM: Pig-tailed macaque
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Query Match
Best Local Similarity 69.5-
The Conservative
                                                                                              4 RCLCRRGVCRCLC 16
                                                                                                                          65 RCICTRGFCRLLC 77
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NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-604-864-1
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Sequence 21. Application US/09309487

Sequence 21. Application US/09309487

Sequence 21. Application Selected, Michael E.

APPLICANT: Selected, Michael E.

APPLICANT: Tung, Yi-Quan

APPLICANT: Van, Jun

APPLICANT: OP INVENTION: Antimicrobial Theta Defensins and Methods of Using Same

FILE REFERENCE: P-UC 3095

CURRENT APPLICANTON NUMBER: US/09/309,487

CURRENT PILIG DATE: 1999-05-10

NUMBER OF SEQ ID NOS: 31

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 21

LENGTH: 92
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Sequence 21, Application US/09967808

Patent No. 6514727

GENERAL INFORMATION:

APPLICANT: Selsted, Michael E.

APPLICANT: Tang, Yi-Quan

APPLICANT: Tang, Yi-Quan

APPLICANT: Tang, Yi-Quan

APPLICANT: Ouellette, Andre J.

TITLE OF INVENTION: Same

TITLE OF INVENTION: Same

TITLE OF INVENTION: Same

CURRENT FILING DATE: 1099/967,808

CURRENT FILING DATE: 1099-26

PRIOR APPLICATION NUMBER: US/09/309,487

PRIOR APPLICATION NUMBER: US/09/309,487

SOFTWARE: PatentIN Ver. 2.0

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 21

INNERH OF 21
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Pred. No. 1.1;
1; Mismatches 3; Indels
                                                                                                                                                                                                                        DB 4; Length 76;
                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                      Score 60; DB 4;
Pred. No. 0.94;
1; Mismatches
NUMBER OF SEQ ID NOS: 125
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LYPE: PRT
ORGANISM: Macaca mulatta
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Best Local Similarity 83.3%;
Matches 10; Conservative
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Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                       4 RCLCRRGVCRCL 15
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US-09-309-487-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRGANISM: Macaca mulatta
                                                                                                                                         ; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-141-645-17
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US-09-967-808-21
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US-09-309-487-21
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                                             Gaps
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Best Local Similarity 62.5%; Pred. No. 0.47;
Matches 10; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hancock, Robert E. W.
APPLICANT: Hancock, Robert E. W.
APPLICANT: And Lijuan
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES AND METHODS OF
TITLE OF INVENTION: USE THEREOF
FILE REPERENCE: USC1170
CURRENT APPLICATION NUMBER: US/09/604,864
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 17
Score 60, DB 4; Length 92;
Pred. No. 1.1;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                              APPLICANT: Robert Lehrer
APPLICANT: Robert Lehrer
APPLICANT: Alexander Cole
APPLICANT: Tareas Hong
TITLE OF INVENTION: Retrocyclins - Antiviral
TITLE OF INVENTION: Antimicrobial Peptides
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-001CIP
CURRENT FILING DATE: 2002-05-06
PRIOR PILING DATE: 2001-04-18
PRIOR PILING DATE: 2001-04-18
PRIOR PILING DATE: 2001-04-18
PRIOR PILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 73
LENGTH: 141
TYPE: PRI
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Pred. No. 1.6;
2; Mismatches
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; CTHER INFORMATION: Xaa = Any Amino Acid
US-10-141-645-73
                                                                                                                                                                                                                              US-10-141-645-73
; Sequence 73, Application US/10141645
; Patent No. 6713078
; GENERAL INFORMATION:
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Sequence 1, Application US/09604864
Patent No. 6337317
GENERAL INFORMATION:
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Best Local Similarity 71.4%;
Matches 10; Conservative
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APPLICANT: Yuan, Jun
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
FILE REFERENCE: P-UC 3095
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Patent No. 6514727
GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Tang, Yi-Quan
APPLICANT: Yuan, Jun
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Annimicrobial Theta Defensins and Methods of Using TITLE OF INVENTION: Same
FILE REFERENCE: P-UC 3095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 180;
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APPLICATION NUMBER: WO PCT/US 96/15774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.9%; Score 57; DB 4;
50.0%; Pred. No. 4.2;
tive 0; Mismatches
                FILING DATE: 06-007-1996

PHILING DATE: 06-007-1996

APPLICATION NUMBER: US 60/004,834

FILING DATE: 05-007-1995

ATTORNEY/AGENT INFORMATION:
NAME: BENETT, DENNIS A

REFERENCE/DOCKET NUMBER: 2910/1

TELEPHONE: 314-694-5402

TELEPHONE: 314-694-9095

INFORMATION FOR SEQ ID NO: 286:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: mino acids
TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; SEQUENCE DESCRIPTION: SEQ ID NO: 286:
US-09-510-238A-286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/309,487
CURRENT FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 20
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20, Application US/09309487; Patent No. 6335318; GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Tang, Yi-Quan
APPLICANT: Yuan, Jun
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100.0%; Pre
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Best Local Similarity 50.0%
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US-09-309-487-20
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Best Local Similarity
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US-09-967-808-20
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APPLICANT ENGLY, CHARLES M
CAPARON, MAIRE H
CAPARON, MAIRE H
ZURFLUH, LINDA L
KLEIN, BARBARA K
MCHHERTER, CHARLES A
SURMERS, NEBAL L
BAUER, S C
LEE, STEPHEN L
AGONISTS
AGONISTS
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MEDIUW TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: TEM PC-DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
COPERATING SYSTEM: PATENTER PA
                                                                                                                                                                                                                                                                      GENERAL INCORMATION:
APPLICANT: THE UNIVERSITY OF BRITISH COLUMBIA
APPLICANT: THE UNIVERSITY OF BRITISH COLUMBIA
APPLICANT: THE UNIVERSITY OF BRITISH COLUMBIA
TITLE OF INVENTION: Lijuan
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES AND METHODS OF
TITLE OF INVENTION: USE THEREOF
TITLE OF INVENTION: USE THEREOF
FILE REPERENCE: USC1170-1
CURRENT FILING DATE: 2002-01-08
PRIOR RILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO :
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 58; DB 4; Length 17; Pred. No. 0.47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Indels
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ADDRESSEE: DENNIS A. BENNETT, G.D. SEARLE & CO.,
CORPORATE FATENT DEPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/09/510,238A
FILING DATE: 22-Feb-2000
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 286, Application US/09510238A Patent No. 6730303 GENERAL INFORMATION:
                                                                                                                                                                                                                Sequence 1, Application US/10042872
Patent No. 6747007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: P.O. BOX 5110
   CRCLCRRGVCRCLCRR 18
                                        2 CFAVCREGRCRYKCRR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 62.5%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Limulus polyphemus US-10-042-872-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 29
US-09-510-238A-286
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Gaps

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Gaps
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                                                                                                                                                                                                                                                                                                                                                        Query Match 50.0%; Score 56; DB 4; Length 9; Best Local Similarity 100.0%; Pred. No. 3.8e+05; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Costructures 121, Application US/10141645

Pacente 121, Application US/10141645

Patent No. 6713078

GENERAL INFORMATION:

APPLICANT: Alan Waring

APPLICANT: Alan Waring

APPLICANT: Alexander Cole

APPLICANT: Teresa Hong

TITLE OF INVENTION: Retrocyclins - Antiviral and

TITLE OF INVENTION: Antimicrobial Peptides

TITLE OF INVENTION: Antimicrobial Peptides

TITLE OF INVENTION: Antimicrobial Peptides

TITLE PEPERENGE: UCLA-001CIP

CURRENT APPLICATION NUMBER: US/10/141,645

CURRENT APPLICATION NUMBER: 60/284,855

PRIOR FILING DATE: 2001-04-18

PRIOR FILING DATE: 2002-04-18

NUMBER OF SEQ ID NOS: 125

SEQ ID NO 121

LENGTH: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 65, Application US/10141645
Patent No. 6713078
GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alexander Cole
APPLICANT: Terest Hong
ITILE OF INVENTION: Retrocyclins - Antiviral and
ITILE OF INVENTION: Antimicrobial Peptides
FILE REPERENCE: UCLA-001C1P;
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT FILING DATE: 2002-05-06
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PRIOR APPLICATION NUMBER: 60/284,855
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 45
LENGTH: 9
                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 RCLCRRGVCRCLCR 17
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Best Local Similarity 64.3
Matches 9; Conservative
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US-10-141-645-121
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US-10-141-645-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL NO. 0.120/0

GENERAL INCORNATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Actimicrobial Peptides
TITLE OF INVENTION: Actimicrobial Peptides
FILE REFERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT APPLICATION NUMBER: 60/284,855
PRIOR FILING DATE: 2002-05-06
PRIOR FILING DATE: 2002-06-06
PRIOR FILING DATE: 2002-06-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 27
LENGTH: 9
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Sequence 45, Application US/10141645
Patent No. 6713078
GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alan waring
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-001CIP
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100.0%; Pred. No. ...
0; Mismatches
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CURRENT FILING DATE: 2002-05-06
       CURRENT APPLICATION NUMBER: US/09/967,808
                              CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US/09/309,487
PRIOR FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27, Application US/10141645
Patent No. 6713078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                              Query Match 50.0
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Macaca mulatta
US-09-967-808-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 RCLCRRGVC 12
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US-10-141-645-27
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APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/094,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32502
LENGTH: 168
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Sequence 40304, Application US/09270767

Sequence 40304, Application US/09270767

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;

FILE REPERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SEQ ID NO 40304

LENGTH: 96
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                                                                                                                                                                                                   Query Match 50.0%; Score 56; DB 4; Length 141; Best Local Similarity 64.3%; Pred. No. 4.5; Matches 9; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 55; DB 4; Length 168; Pred. No. 6.8;
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Best Local Similarity 47.4%; Pred. No. 4.9;

Matches 9; Conservative 3; Mismatches 4;
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PRIOR FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 1.25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 32502, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 CRCLCRR---GVCRCLCRR 18 | | | | | | | |
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ORGANISM: Pseudomonas aeruginosa
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69 RCICGRGICRLLRR 82
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Best Local Similarity 66.7°
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                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-252-991A-32502
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                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-17-141-042-05
) Sequence 69, Application US/10141645
) Patent No. 6713078
) GENERAL INFORMATION:
APPLICANT: ROBERT Lehrer
APPLICANT: Alam Waring
APPLICANT: Alaxander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral
TITLE OF INVENTION: Antimicrobial Peptides
FILE REPRENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT FILING DATE: 2002-06-06
) PRIOR FILING DATE: 2002-04-18
) PRIOR FILING DATE: 2002-04-08
) PRIOR FILING DATE: 2002-04-08
) RIOR APPLICATION NUMBER: Unassigned
) PRIOR FILING DATE: 2002-04-18
) ROMER OF SEQ ID NOS: 125
SOFTWARE: FREESEQ for Windows Version 4.0
) ENGURENT HONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 125, Application US/10141645

Patent No. 6713078

GENERAL INDEMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
TITLE REFERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT FILING DATE: 2002-05-06
PRIOR PILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: Unassigned
PRIOR APPLICATION NUMBER: 60/284,855
PRIOR FILING DATE: 2001-04-18
PRIOR PLILNG DATE: 2001-04-18
PRIOR APPLICATION NUMBER: Unassigned
PRIOR PILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 65
LENGTH: 140
TYPE: PRT
ORGANISM: Home sapiens
US-10-141-645-65
                                                                                                                                                                                                                                                                                                                          2; Mismatches
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Best Local Similarity 64.3
Matches 9; Conservative
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Matches 9; Conservative
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ORGANISM: Gorilla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-10-141-645-125
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                                                                                                                                                                                                                                                                             Query Match
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g
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RESULT 40

US-09-270-767-55520

Sequence 55520, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT PATENTE PATENTING DATE: 1999-03-17

SOFTWARE: Patentin Ver. 2.0

LENGTH: 96

TYPE: PRT

CREANISM: Drosophila melanogaster

CS-09-270-767-55520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 47.4%; Pred. No. 4.9;
Matches 9; Conservative 3; Mismatches 4; Indels
16 CGCVCQRRCAGVCACECSK 34
```

1;

3; Gaps

Search completed: October 26, 2004, 15:41:19 Job time : 32.5 secs

3 CRCLCRR---GVCRCLCRR 18 | | : | : | | | | | : 16 CGCVCQRRCAGVCACECSK 34

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T.

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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; Search time 23.5 Seconds (without alignments) 73.698 Million cell updates/sec OM protein - protein search, using sw model October 26, 2004, 15:15:31 Run on:

US-10-009-317A-33 112 1 GVCRCLCRRGVCRCLCRR 18 Title: Perfect score: Sequence:

283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARIES

	Description	theta defensin-1	theta defensin 1b	ical	ical	endc	Н	ical		hypothetical prote	ical	membran	probable integral	G protein-coupled	AcOrf-70 protein -	hypothetical prote	걁	pt	Balbiani ring 3 pr	genome polyprotein	otogelin - mouse	Q300 protein - mou	terol is	nel protein - chic	neurotoxin Tx2 - s	pulmonary surfacta	fibronectin recept	hypothetical prote	chloramphenicol re	probable diogenase
SUMMARIES	ID	1 80	B59089	T15651	T24272	869207	T15617	T18975	A59089	T48125	B45878	S50807	E71602	JC5042	G72858	B70554	EGMSMG	A41116	S08167	GNNY21	T42214	I48725	687	0	S29214		C37057	D72481	ສ	H90942
	DB	2	N															7	~	Н	~	N	7	7	~	н	N	7	N	7
	Length	18	94	188	164	419	1131	152	76	82	582	131	248	476	290	303	1217	265	1700	2206	2910	77	256	835	53	79	94	128	302	321
о¥	강성	Ϊ.;	53.6	51.8	。	7		•	•	ů.	45.1	•	4.	ω,	N.	42.9	ď	ď	٠.	~	ď.	•	ä	41.5	•	•	٠	٠	٠	41.1
	Score	80	9	58	57	53.5	'n.	52	51	51	50.5	. 20	49.5	49	48	48	48	47.5	47	47	47		46.5	ů.	46	46	46	46	46	46
			7	٣	4	ß	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	20

VANCESSION: D23/02.
VANCESSION: D23/02.
VANCESSION: D23/02.
VANCESSION: D23/02.
VANCESSION: D23/02.
VANCESSION: SECONDIAL
VALUE: A CYCLIC antimicrobial peptide produced in primate leukocytes by the ligation of
A,Reference number: A59089.
MUD:99453140; PMID:10521339
A,Rocession: B59089
A,Status: preliminary
A,Rolecule 'Ype: man,A
A,Residues: L-76 «TANA
A,Residues: L

probable dioxygena	probable diogenase	cobyric acid synth	epidermal growth f	restrictin precurs	proteinase inhibit	Bowman-Birk protei	proteinase inhibit	hypothetical prote	hypothetical prote	probable dioxygena	probable cobQ prot	protein F12K21.20	fibronectin recept	hypothetical prote	hypothetical prote
C64941	D85791	C82426	EGRT	JH0675	807405	JC2225	TISYC2	T28784	S02186	AE0304	C70940	H86468	B27079	T15840	826689
7	0	N	н	Н	~	N	Н	~	~	N	0	N	7	0	0
321	321	484	1133	1353	83	94	103	532	95	321	494	602	798	2946	118
41.1	41.1	41.1	41.1	41.1	40.6	40.6	40.6	40.6	40.2	40.2	40.2	40.2	40.2	40.2	39.7
46	46	46	46	46	45.5	45.5	45.5	45.5	45	45	45	45	45	45	44.5
30	31	32	33	34	35	36	37	38	6 E	40	41	42	43	44	45

## ALIGNMENTS

Oy 4 RCICTRGFCRCACRR 18  Db 1 RCICTRGFCRCACRR 15  RESULT 2  RESULT 2  The a defensin 1b precursor - rhesus macaque	Query Match 71.4%; Score 80; DB 2; Length 18; Best Local Similarity 80.0%; Pred. No. 0.0015; Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	A.Title: 20, 130-120, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20, 130-20,	RESULT 1 C159089 that defensin-1 - rhesus macaque N;Alternate names: RTD-1 C;Species: Macaca mulatta (rhesus macaque) C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C;Date: 29-Oct-1990 #sequence_revision 29-Oct-1999 K.; Tran, D.; Miller, C.J.; Ouellette, A.J.; R;Pang, Y.Q.; Yuan, J.; Osapay, G.; Osapay, K.; Tran, D.; Miller, C.J.; Ouellette, A.J.;
Query Match 71.4%; Score 80; DB 2; Length 18; Best Local Similarity 80.0%; Pred. No. 0.0015; Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps		אינעמלסרטט: T-TO לפפר	Science 286, 498-502, 1999 A;Title: A cyclic antimicrobial peptide produced in primate leukocytes by the ligation of A;Areference number: A59089; WUID:99453140; PMID:10521339 A;Accession: C59089 A;Status: preliminary A;Acteus: preliminary A;Status: preliminary A;Batus: preliminary A;Batus: 118, AFF.

Query Match

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A; Regidues: 1.419 <-000>
A; Cross-references: UNIPROT: P49767; EMBL: X94216; NID: 91177488; PIDN: CAA63907.1; PID: e2216
A; Cross-references: UNIPROT: P49767; EMBL: X94216; NID: 91177488; PIDN: CAA63907.1; PID: e2216
A; Cross-references: UNIPROT: P49767; EMBL: X94216; NID: 91177488; PIDN: CAA63907.1; PID: e2216
A; Note: this is a revision to the sequence from reference S61795
A; Note: this is a revision to the sequence from reference S61795
BMBO J: 15, 290-298
A; Title: A novel vascular endothelial growth factor, VEGF-C, is a ligand for the Flt4 (VEA; A; Accession: S61795
A; Reference number: S61795; MUID: 96178224; PMID: 8617204
A; Molecule type: many
A; M
vascular endothelial growth factor C precursor - human
N;Alcernate names: FLT4 ligand DHM
C;Species: Alfono sobiens (man)
C;Species: Alfono sobiens (man)
C;Date: 27-Apr-1996 #sequence revision 01-Nov-1996 #text_change 09-Jul-2004
C;Accession: S69207; S61795; S71443; S69208; G02659
C;Accession: S69207; S61795; S71443; S69208; G02659
BMBO J. 15, 1151, 11996
A;Title: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand for A;Reference number: S69207; MUID:96203094; PMID:8612600
A;Accession: S69207
A;Accession: S69207
A;Amolecule type: mRNA
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 'X', 104-120 «JOUZ»
A;Lee, J.; Gray, A.; Yuan, J.; Luoh, S.M.; Avraham, H.; Wood, W.I.
Submitted to the EMBL Data Library, December 1995 .
A;Description: Vascular endothelial growth factor related protein (VRF): A ligand and spe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Cross-references: GDB:3890883; OMIM:601528
F;1-12/Domain: signal sequence #starus predicted <SIG>
F;1-102/Domain: propeptide #starus predicted <PRO>
F;10-419/Product: vascular endothelial growth factor C #starus experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:U43142; NID:g1150988; PIDN:AAA85214.1; PID:g1150989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein C25F6.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15617
S;Bentley, D.
Submitted to the EMBL Data Library, October 1995
A;Bescription: The sequence of C. elegans cosmid C25F6.
A;Reference number: Z18377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Status: preliminary, translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-419 <MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 14;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291 CQCVCRAGLRPASCGPHKELDRNSCQCVCK 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Morris, J.C.
submitted to the EMBL Data Library, May 1996
A;Reference number: H01557
A;Accession: G02659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 26.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 CRCLCRRGV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-419 < LEE>
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A;Reference number: 219867
A;Accession: T24272
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-164 <MILD.
A;Cross-references: UNIPROT: Q22048; EMBL: Z66499; PIDN: CAA91301.1; GSPDB: GN00020; CESP: Td
A;Experimental source: clone T01B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Kesidues: 1-188 cNHA>
A;Kesidues: 1-188 cNHA>
A;Cross-references: UNIPROT:Q18238; EMBL:U58760; NID:g1330384; PID:g1330389; PIDN:AABO07
A;Experimental source: strain Bristol N2; clone C27A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein C27A2.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24272
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                F;21-64/Domain: amino-terminal propeptide #status predicted <PRO> F;74-76/Domain: carboxyl-terminal propeptide #status predicted <CTP>
                                                                                                                                                                                                        ;
0
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0
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                                                                                                                        Score 60; DB 2; Length 76;
Pred. No. 0.81;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rinhan, M. submitted to the EMBL Data Library, May 1996 A;Description: The sequence of C. elegans cosmid C27A2. A;Reference number: Z18382 A;Reference number: Z18382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein T01B7.8 - Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 58; DB 2;
Pred. No. 2.4;
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Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GVCRCLCRRGVCRCLCRR 18
                                                                                                                            53.6%;
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Best Local Similarity 55.6%;
Matches 10; Conservative
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Best Local Similarity 55.6
Matches 10; Conservative
                                                                                                                                                                Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                 65 RCLCRRGVCQLL 76
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A,Map position: 2
A;Introns: 19/3; 91/2
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A; Map position: 2
A; Introns: 20/3; 90/2
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65 RCICTRGFCRLL 76

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2; Indels

11arity 47.1%; Score 52.5; Conservative 4; Mismatches

Query Match Best Local Similarity Matches 8; Conservē

2 VCRCLCRRGVCRCLCRR 18

hypothetical protein C06A1.6 - Caenorhabditis elegans

A; Molecule type: DNA

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Probable membrane protein YJL064w - yeast (Saccharomyces cerevisiae)
N.Alternate names: hypothetical protein HRC131; hypothetical protein J1120
C,Species: Saccharomyces cerevisiae
C,Species: Saccharomyces cerevisiae
C,Species: Sacharomyces cerevisiae
C,Species: Sacharomyces cerevisiae
R,Vandenbol, M.; Durand, P.; Dion, C.; Portetelle, D.; Hilger, F.
Yeast 11, 57-60, 1995
A,Title: Sequence of a 17.1 kb DNA fragment from chromosome X of Saccharomyces cerevisiae
A,Reference number: S50798; MUID:95282514; PMID:7762302
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R;Sarvetnick, N.; Tsai, J.Y.; Fox, H.; Pilder, S.H.; Silver, L.M.
Rmunogenetics 30, 34-41, 1989
A;Title: A mouse chromosome 17 gene encodes a testes-specific transcript with unusual procedence number: A45878; MUID:89307395; PMID:2568335
                                                                                                                                                                                                                                                                                                           R;Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ij
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A;Residues: 1-582 <SAR>
A;Cross-references: UNIPROT:Q62295; GB:M28821
A;Note: this sequence has been corrected in Immunogenetics 31, 283-284 (1990)
C;Superfamily: mouse hypothetical protein 2
                                                                                                                                                            hypothetical protein F16M2.210 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein 2 - mouse
C,Species: Mus musculus (house mouse)
C,Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.5%; Score 51; DB 2; Length 85; 44.4%; Pred. No. 9.6;
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A;Molecule type: DNA
A;Residues: 1-85 <RIE>
A;Cross-references: UNIPROT:Q9M1V4; EMBL:AL138648
A;Experimental source: cultivar Columbia; BAC clone F16M2
C;Genetics:
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Best Local Similarity 56.2%; Pred. No. 37;
Matches 9; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.4%; Prec. ....+ive 2; Mismatches
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Best Local Similarity
Matches 12; Conserv
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A;Introns: 20/1
A;Note: F16M2.210
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C;Superfamily: mammalian defensin
C;Superfamily: mammalian defensin
C;Superfamily: mammalian defensin
F;1-20/Domain: signal sequence #status predicted <SIG>F;1-20/Domain: signal sequence #status predicted <SIG>F;21-64/Domain: amino-terminal propeptide #status predicted <PRO>F;74-76/Domain: carboxyl-terminal propeptide #status predicted <CIP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rimcharray, A.

Submitted to the EMBL Data Library, June 1995

A; Accession: T18975

A; Actual: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: DNA

A; Residues: 1-152 < WILL>
A; Residues: UNIPROT: Q9XVX3; EMBL: Z49886; PIDN: CAA90055.1; GSPDB: GN00020; CESP: CC
A;Residues: 1-1131 <BEN>
A;Cross-references: EMBL:U39742; NID:g1049455; PID:g1049459; PIDN:AAA80434.1; CESP:C25F9
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                                                                       C;Genetics:
A;Gene: CESP:C25F6.2
A;Introns: 105/1; 210/3; 283/3; 316/1; 346/2; 463/3; 566/1; 722/2; 897/1; 991/2; 1032/1;
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CiDate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
CiAccession: T18975
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Length 152;

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Score 52; DB 2 Pred. No. 11; 0; Mismatches

A, Experimental source: clone C06A1

A,Gene: CESP:C06Al.6 A,Map position: ?

; 0

Query Match
Best Local Similarity 52.9%;
Matches 9; Conservative (

1 GVCRCLCRRGVCRCLCR 17

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67 GGCGCCCRPRCCCCCR 83

8; Indels

Query Match
Best Local Similarity 66.7%; Pred. No. 8.9;
Matches 8; Conservative 1; Mismatches 3; Indels

A; Accession: A59089 A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-76 < TAN>

4 RCLCRRGVCRCL 15

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hypothetical protein Rv1145 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Accession: B70554
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.S.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sullston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome & A;Reference number: A70500; MUID:98295987; PMID:9634230
                         A;Residues: 1-476 <ISO>
A;Cross-references: UNIPROT:Q93126; DDBJ:D78363; NID:g1514430; PIDN:BAA11375.1; PID:g1514
C;Superfamily: vertebrate rhodopsin
                                                                                                                                              C;Rejwords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prote
F;34-57/Domain: transmembrane #status predicted <TMl>
F;71-93/Domain: transmembrane #status predicted <TM2>
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A.Cross-references: UNIPROT:006545; GB:Z95584; GB:AL123456; NID:g3261774; PIDN:CAB09033.3
A.Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F:13,17/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:230,240,250,260/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status
F:355/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predict
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A,Residues: 1-290 <AXR>
A,Cross-references: UNIPROT:P41470; GB:L22858; NID:G510708; PIDN:AAA66700.1; PID:G559139
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                                                                                                                                                                                                                                                           F;107-129/Domain: transmembrane #status predicted <TM3>F;126-134/Region: G protein-binding #status predicted F;148-172/Domain: transmembrane #status predicted <TM4>F;149-222/Domain: transmembrane #status predicted <TM4>F;377-398/Domain: transmembrane #status predicted <TM5>F;377-398/Domain: transmembrane #status predicted <TM5>F;407-430/Domain: transmembrane #status predicted <TM5>F;407-430/Domain: transmembrane #status predicted <TM7>F;407-430/Domain: transmembrane #status predicted <TM7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 49; DB 2;
Pred. No. 49;
3; Mismatches
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Pred. No. 47;
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442 LCKCVCRRGAMERRFRR 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 43.8%;
Similarity 47.1%;
8; Conservative
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ilarity 52.9%;
Conservative
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Rest Local Similarity
9; Conserve
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Best Local Similarity
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                         A;Cross-references: UNIPROT:P47038; EMBL:Z34288; NID:9498992; PIDN:CAA84058.1; PID:94990
A;Note: the nuclectide sequence was submitted to the EMBL Data Library, June 1994
R;Vandenbol, M.; Durand, P.; Dion, C.; Portetelle, D.; Hilger, F.
submitted to the EMBL Data Library, June 1994
A;Description: Sequence analysis of a 17.1 kb DNA fragment from chromosome X of Sacchard
A;Reference number: 847117
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R;Isoai, A.; Kawahara, H.; Okazaki, Y.; Shizuri, Y.
Gene 175, 95-100, 1996
A;Title: Molecular cloning of a new member of the putative G protein-coupled receptor ge A;Reference number: JCS042; MUID:97074655; PMID:8917082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable integral membrane protein PFB0950w - malaria parasite (Plasmodium falciparum) (Species: Plasmodium falciparum (S.Species: Plasmodium falciparum (S.Species: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004 (S.Accession: E71602 ** R.J.*, Tettellin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, B.V.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O. Science 282, 1126-1132, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Residues: i-248 «GAR»
Cross-references: UNIPROT:096282; GB:AE001428; GB:AE001362; NID:93845316; PIDN:AAC7197;
Experimental source: clone 3D7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Accession: E71602
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C;Species: Balanus amphitrite (barnacle)
C;Date: 21-Jan-1997 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: EMBL:Z49340; NID:g1008212; FID:g1008214; MIPS:YJL064w
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C;Superfamily: Saccharomyces probable membrane protein YJL064w
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 131
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                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-131 «VAM».
A; Cross-references: EMBL: Z34288; NID: 9498922; PID: 9499002
R; Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
submitted to the Protein Sequence Database, September 1995
A; Reference number: S56835
A; Accession: S56838
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17;
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Pred. No. 28
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Pred. No. 1
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Best Local Similarity 52.9%;
Matches 9; Conservative
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Best Local Similarity 46.7%;
Matches 7; Conservative
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A;Residues: 1-131 <VAN>
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transcription factor AMT1, metal-inducible - yeast (Candida glabrata)
C;Species: Candida glabrata
C;Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 09-Jul-2004
C;Accession: A41116
R;Zhou, P.; Thiele, D.J.
Proc. Natl. Acad. Sci. U.S.A. 88, 6112-6116, 1991
A;Ttle: Isolation of a metal-activated transcription factor gene from Candida glabrata b A;Reference number: A41116; MUID:91296771; PMID:2068090
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C;Species: Chironomus tentans
C;Species: Chironomus tentans
C;Accession: S08167
R;Paulsson, G.; Lendahl, U.; Galli, J.; Ericsson, C.; Wieslander, L.
J,Mol. Biol. 211, 331-349, 1990
A;Rtle: The balbiani ring 3 gene in Chironomus tentans has a diverged repetitive structh A;Reference number: S08167; MUD: 90172404; PMID:1689777
A;Accession: S08167 with conceptual translation
A;Reture compared with conceptual translation
A;Molecule type: DNA
                             F:530-572/Domain: LDL receptor YWTD-contraining repeat homology <YW08>
F:573-615/Domain: LDL receptor YWTD-contraining repeat homology <YW09>
F:616-60-700-70main: LDL receptor YWTD-contraining repeat homology <YW10>
F:60-700/Domain: LDL receptor YWTD-contraining repeat homology <YW11>
F:60-700/Domain: LDL receptor YWTD-contraining repeat homology <YW12>
F:701-743/Domain: EGF homology <EG5>
F:842-875/Domain: EGF homology <EG8>
F:842-875/Domain: EGF homology <EG8>
F:923-958/Domain: EGF homology <EG8>
F:923-958/Domain: EGF homology <EG8>
F:977-1029/Product: epidermal growth factor #status experimental <EGF>
F:982-1018/Domain: EGF homology <EG8>
F:1039-1063/Domain: transmembrane #status predicted <TWM>
F:1064-1217/Domain: intracellular #status predicted <INT>
F:1064-1217/Domain: intracellular #status with the first of the firs
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A,Residues: 1-265 <ZHO>
A,Cross-references: UNIPROT:P41772; GB:M69146; NID:g173319; PIDN:AAA35271.1; PID:g173320
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A;Cross-references: UNIPROT:Q03376; GB:X52263; NID:g7057; PIDN:CAA36506.1; PID:g7058
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66.7%; Pred. No. 50;
tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 42.9%; Score 48; DB 1; Length 1217; Best Local Similarity 47.4%; Pred. No. 1.2e+02; Matches 9; Conservative 2; Mismatches 6; Indels
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Pred. No. 1.9e+02;
repeat
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22.6%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Molecule type: mRNA
A; Moestudes: 1-789,'Y', 791-1047,'S',1049-1168 cGRA>
A; Motes the sequence shown by these authors differs from residues 1134-1168 due to an intence of Scott et al.)
A; Note: the sequence shown by these authors differs from residues 1134-1168 due to an intence of Scott et al.)
B; Savage Jr., C.R.; Inagami, T.; Cohen, S.
J. Biol. Chem. 247, 7612-7621, 1972
J. Siol. Chem. 247, 7612-7621, 1972
A; Title: The primary structure of epidermal growth factor.
A; Reference number: A92118; MUID:73048516; PMID:4636327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Comment: Epidermal growth factor (EGF) stimulates the proliferation and differentiation gastrointestinal cell proliferation.

C.Comment: EGF is released in the pancreas, small intestine, mammary gland, and (in some C.Comment: EGF is released in the pancreas, small intestine, mammary gland, and (in some C.Comment: The EGF precursor is found in kidney as a receptor-like membrane-bound protein C.Comment: The active growth factor from this submaxillary gland protein stimulates the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-1217 <SCO>
A;Cross-references: UNIPROT:P01132; GB:J00380; NID:g192993; PIDN:AAA37539.1; PID:g309216
R;Gray, A.; Dull.; T.; Ullrich, A.
R;Gray, A.; Dull.; T.; Ullrich, A.
A;Title: Nucleotide sequence of epidermal growth factor cDNA predicts a 128,000-molecula
A;Reference number: A93304; MUID:83219309; PMID:6304537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A) Aletermal growth factor precursor - mouse (N) Alternate names surgestrone precursor (S) Alternate names undesstrone precursor (S) Alternate names undesstrone precursor (S) Alternate names undesstrone precursor (S) Date: 30-Nov-1980 #sequence_revision 11-Aug-1983 #text_change 09-Jul-2004 (C) Accession: A) Ag121, A) A3314; 
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A; Residues: 977-1029 <SAV>
A; Residues: 977-1029 <SAV>
A; Residues: 977-1029 <SAV>
A; Note: residues: 1024-1029 <SAV>
B; Savage Jr., C.R.; Hash, J.H.; Cohen, S.
J. B; Ol. Chem. 248, 7669-7672, 1973
J. B; Ol. Chem. 248, 7669-7672, 1973
A; Title: Epidermal growth factor. Location of disulfide bonds.
A; Reference number: A92144; MUID:7402498; PMID:4750422
A; Contents: annotation; disulfide bonds.
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                                                                                                                                                                                                                                                                                     Gaps
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0
                                                                                                                                                                           Length 303;
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                                                                                                                                                                     Score 48; DB Pred. No. 48; 0; Mismatches
                                                                                                                                                                           42.9%;
ilarity 60.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     4 RCLCRRGVCRCLCRR 18
                                                                                                                                                                     Query Match
Best Local Similarity
Matches 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A93304
     C,Genetics:
A,Gene: Rv1145
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G100 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Uul-1996 #sequence_revision 02-Uul-1996 #text_change 09-Jul-2004
C;Date: 02-Uul-1996 #sequence_revision 02-Uul-1996 #text_change 09-Jul-2004
C;Date: 02-Uul-1996 #sequence_revision 02-Uul-1996 #text_change 09-Jul-2004
C;Datession 148725
A;Reference number: 148725; MUID:91237845; PMID:1851876
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CjSpecies: Gallus gallus (chicken)
CjSpecies: Gallus gallus (chicken)
CjSpecies: Gallus gallus (chicken)
CjSpecies: Gallus gallus (chicken)
CjSpecies: Jage #sequence_revision 24-Feb-1995 #text_change 04-Apr-2004
CjAccession: A38963; JP0076
RjMatsuhashi, S.; Noji, S.; Koyama, E.; Myokai, F.; Ohuchi, H.; Taniguchi, S.; Hori, K.
BjMatsuhashi, S.; Noji, S.; Koyama, E.; Myokai, F.; Ohuchi, H.; Taniguchi, S.; Hori, K.
AjMatsuhashi, S.; Noji, S.; Koyama, B.; Myokai, F.; Ohuchi, H.; Taniguchi, S.; Hori, K.
AjMileula (New gene, nel, encoding a Mr 93K protein with EGF-like repeats is strongly expre
AjAccession: A38963
AjAccession: A38963
AjAccession: A38963
AjAccession: B355 (MAI)
AjCross-references: DDBJ:D45365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-77 <RDS
A;Cross.references: UNIPROT:Q02722; EMBL:X52164; NID:G53860; PIDN:CAA36417.1; PID:G53861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-8 srerol isomerase (EC 5.3.3.-) [imported] - Neurospora crassa NiAlternate names: delta 8 ->delta 7 sterol isomerase (5.5pecies: Neurospora crassa C;Species: Neurospora crassa C;Cpecies: Mar-2000 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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A.Introns: 145/1
C.Keywords: intramolecular oxidoreductase; isomerase; sterol biosynthesis
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A;Cross-references: UNIPROT:Q92254; EMBL:U59671; PIDN:AAB09470.1
A;Experimental source: strain OR23-74-1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 77;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 64;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 41.5%; Score 46.5; I Best Local Similarity 53.3%; Pred. No. 30; Matches 8; Conservative 2; Mismatches
724 CRRDACRCGQPCLCATLAHYARLCRR 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C, Accession: T46871
R,Gilbert, J.; Orbach, M.J.
submitted to the EMBL Data Library, May 1996
A, Reference number: 224117
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Best Local Similarity 66.7%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 VCVCVC---VCVCVC 38
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; Residues: 1-2206 4HUG>
; Residues: 1-2206 4HUG>
; Cross-references: UNIPROT: P22055; GB: D00538; NID: G221147; PIDN: BAA00426.1; PID: G221148
; Cross-references: UNIPROT: P22055; GB: D00528; NID: G221147; PIDN: BAA00426.1; PID: G221148
; Reywords: coat protein; core protein; genome-linked protein; nucleotidyltransferase; p. 1-69/Product: coat protein IA #status predicted < VP2>
; 340-578/Product: coat protein IC #status predicted < VP2>
; 347-578/Product: coat protein ID #status predicted < VP2>
; 379-881/Product: coat protein ID #status predicted < VP1>
                                                                                                                                                                                                                                                                                                       genome polyprotein - coxsackievirus A21 (strain Coe)
N;Contains: coat protein 1A; coat protein 1B; coat protein 1C; coat protein 1D; core pro
polymerase (EC 2.7.7.48)
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(Cross-references: UNIEROT:055225; EMBL:U96411; NID:g2760883; PID:g2760884; PIDN:AAB965)
(Experimental source: strain BALB/c
:Note: component of all the acellular membranes of the inner ear
:Note: component of all the acellular membranes of the inner war
:Note: component of all the acellular membranes of the inner war
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roc. Natl. Acad. Sci. U.S.A. 94, 14450-14455, 1997
;Title: Otogelin: A glycoprotein specific to the acellular membranes of the inner ear.; Reference number: Z22079; MUID:98070772; PMID:9405633
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Alternate names: mucin-like extracellular matrix protein
Species: Mus musculus (house mouse)
Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2004
   Gaps
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F;1541-1562/Product: genome-linked protein VPG #status predicted <PB3>
F;1563-1745/Product: proteinase #status predicted <PC3
F;1746-2206/Product: RNA-directed RNA polymerase #status predicted <PD3
F;1746-2206/Product: RNA-directed RNA polymerase #status predicted <PD3
F;1543/Binding site: phosphoryl-RNA (Tyr) (covalent) #status predicted
   16;
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Best Local Similarity 52.9%; Pred. No. 2.2e+02;
Matches 9; Conservative 1; Mismatches 7; Indels
   Indels
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1126-1453/Product: core protein 2C #status predicted <PC2>
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Molecule type: mRNA
                                                                                                                                     1245 CRCVCPKNMEKPADNCKTKWWNDEMCQCVCK 1275
   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           931 IARCSCRCGVYYCESRR 947
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: coxsackievirus A21
                                                                    3 CRCLCRRG----
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Matches
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Cispecies: Aeropyrum pernix
Cibate: 20-Aug-1999 #text_change 09-Jul-2004
Cibate: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
Cibate: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
Rixawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahe awa, H.; Takamiya, M.; Masuda, B.; Funahashi, T.; Tanaka, Y.; Gidoh, Y.; Yamazaki, J.; K. DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyru A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: D72481
A;Accession: D72481
A;Accession: D72481
A;Accession: D12481
A;Accessi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Species: Cavia porcellus (guinea pig)
C.Date: 15-Feb-1991 #sequence_revision 15-Feb-1991 #text_change 16-Aug-2004
C.Date: 15-Feb-1991 #sequence_revision 15-Feb-1991 #text_change R.
C.Date: 15-Feb-1991 #sequence_revision 15-Feb-1991 #text_change R.
C.Date: 15-Feb-1991 #sequence_revision 15-Feb-1991 #text_change R.
C.Date: 15-Feb-1991 #sequence_revision revision 15-Feb-1991 #text_change R.
C.Saperfeaminary: not compared with conceptual translation
A.Residues: 1-94 CSHE>
A.Residues: 1-94 CSHE>
C.Superfeamily: Integrin beta chain; laminin-type EGF-like homology
C.Superfamily: Integrin beta chain; heterodimer; membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R.Dorman, C.J.; Foster, T.J.; Shaw, W.V.
Gene 41, 349-353, 1986
A,Title: Nucleotide sequence of the R26 chloramphenicol resistance determinant and identi
A,Reference number: A25854; MUID:86221720; PMID:3011609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ٦;
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C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C;Accession: A25654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Best Local Similarity 47.6%; Pred. No. 47;
Matches 10; Conservative 2; Mismatches 5; Indels
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Pred. No. 39;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fibronectin receptor beta chain - guinea pig (fragment)
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Best Local Similarity 57.1%;
Matches 8; Conservative
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44 GICQCLAERYIVICL 58
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                                      GVCRCLCRRGVCRCL
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A; Gene: APE2492
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N.Alternate names: low molecular mass surfactant protein type 1
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: 500363
R;Curstedt, T.; Johansson, J.; Barros-Soederling, J.; Robertson, B.; Nilsson, G.; Westbe Bur. J. Blochem. 172, 521-525, 1998
A;Rieferencem. Indeedlar mass surfactant protein type 1. The primary structure of a hydrop and the primary struct
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C;Species: Phoneutria nigriventer
C;Species: Phoneutria nigriventer
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
R;Accompanion: Solderion, M.; Ribeiro Diniz, C.; do Carmo Valentim, A.; von Eickstedt, V FEBS Lett. 310, 153-156, 1992
FEBS Lett. 310, 153-156, 1992
A;Title: The purification and amino acid sequences of four Tx2 neurotoxins from the venc A;Reference number: S29214; MUD:93011905; PMID:1397265
A;Accession: S29214
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                         Appearable shi, S.; Noji, S.; Koyama, E.; Myokai, F.; Ohuchi, H.; Taniguchi, S.; Hori, K. submitted to JIPID, January 1995

submitted to JIPID, January 1995

submitted to JIPID, January 1995

Appearable of JIPID, JIPID,
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Local Similarity 50.0%; Pred. No. 1.4e+02;
hes 9; Conservative 1; Mismatches 3; Indels
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41.1%; Score 46; DB 2; Length 53;
Best Local Similarity 34.6%; Pred. No. 27;
Matches 9; Conservative 2; Mismatches 5; Indels
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41.1%; Score 46; DB 1; Length 79;
Best Local Similarity 46.7%; Pred. No. 35;
Matches 7; Conservative 3; Mismatches 5; Indels
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A;Residues: 1-79 «CUR»
A;Coss-references: UNIROT:P15782
C;Comment: Pulmonary surfactant prote
C;Superfamily: pulmonary surfactant profe;
C;Reywords: alveolar proteinosis; gae
F;1-79/Domain: saposin repeat homology
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A; Experimental source: 9-day embryo
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A, Molecule type: protein
A, Residues: 1-53 <COR>
C, Superfamily: curtatoxin
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Best Local
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epidermal growth factor precursor - rat
N;Alternate names: urogastrone precursor
C;Species: Rattus norvegicus (Norway rat)
                                                                                                  CLCREGVC 275
                                               CLCRRGVC 12
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EGRT
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A;Accession: A25854
A;Molecule type: DNA
A;Residues: 1-302 <DOR>
A;Cross-references: UNIPROT:P12056; GB:M22614; NID:g151802; PIDN:AAA26079.1; PID:g151803
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Status: preliminary
A.Moleoule type: DNA
A.Residues: 1-321 <HAY>
A.Cross-references: UNIPROT: CBXDR8; GB:BA000007; PIDN:BAB35935.1; PID:gl3361979; GSPDB:G
A.Experimental source: strain O157:H7, substrain RIMD 0509952
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Cispecies: Escherichia coli
Cispecies: Escherichia coli
Cipace: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 16-Aug-2004
CiAccession: C64941
Respective: F.R., Plunkert III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
Science 277, 1453-1462, 1997
A; Rese, D.J.; Mau, B.; Shao, Y.
A; Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: H90942
C;Accession: H90942
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             robable diogenase beta subunit [imported] - Bscherichia coli (strain 0157:H7, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Genetics:
A;Gene: EC$2512
C;Superfamily: phthalate dioxygenase reductase; cytochrome-b5 reductase homology; ferred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: UNIPROT:P76254; GB:AE000274; GB:U00096; NID:g1788089; PIDN:AAC74873.
Experimental source: strain K-12, substrain MG1655
Superfamily: Phthalate dioxygenase reductase; cytochrome-b5 reductase homology; ferred
11-225/Domain: cytochrome-b5 reductase homology <CBR>
5254-309/Domain: ferredoxin [2Pe-2S] homology <FRR>
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                                                                                                                                                                                                                                                                                                                                                           Gaps
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41.1%; Score 46; DB 2; Length 321;
Best Local Similarity 87.5%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 1; Indels
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Pred. No. 82;
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Pred. No. 85;
0; Mismatches
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 57.1%; Pred. No. 82;
Matches 8; Conservative 2; Mismatches
                                                                                                                                                                             A;Genome: plasmid
C;Superfamily: bicyclomycin resistance protein
C;Keywords: antibiotic resistance
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Best Local Similarity 87.5%;
Matches 7; Conservative
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35 CVSRFGHDRCICRR 48
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Cobyric acid synthase VCA0727 [imported] - Vibrio cholerae (strain Ni6961 serogroup O1) C; Species: Vibrio cholerae (c) Date: 118-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 (c) Accession: G162426 #sequence_revision, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; R. R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000 *Affile: Nh. Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A; Reference number: A82035; MUID:20406833; PMID:10952301
probable diogenase beta subunit yeax [imported] - Escherichia coli (strain O157:H7, subst
C.Species: Escherichia coli
C.Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Aug-2004
                                                                                                  C;Accession: D85791
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, Iller, L.; Grobbeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q8XDR8; GB:AE005174; NID:g12515843; PIDN:AAG56792.1; GSPDB:GN
A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: yeaX
C;Superfamily: Phthalate dioxygenase reductase; cytochrome-b5 reductase homology; ferredd
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A;Experimental source: serogroup Ol; strain N16961; biotype El Tor
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Pred. No. 85;
0; Mismatches 1; Indels
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Pred. No. 1.1e+02;
2; Mismatches 4; Indels
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A,Map position: 2
C,Superfamily: probable cobyric acid synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative
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Best Local Similarity 57.1%;
Matches 8; Conservative 2
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restrictin precursor - chicken
Cispedies: Gallus gallus (chicken)
Cispedies: Gallus gallus (chicken)
Cipate: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
Cipacession: JH0675; P80385; $23254
Cipacession: JH0675; P80385; $23254
Noremberg, U.; Wille, H.; Wolff, J.M.; Frank, R.; Rathjen, P.G.
Neuron 8, 849-863, 1992
A; Thle: The Chicken neural extracellular matrix molecule restrictin: similarity with EGF
A; Reference number: JH0675; WUID:92265288; PMID:1375037
                                                                                                                                                                                                                                                                           F;1036-1060/Domain: transmembrane #status predicted <TWM>
F;1061-1133/Domain: intracellular #status predicted <INT>
F;342-355,361-372,368-381,383-396,402-413,409-422,424-437,440-452,448-462,464-477,747-758
-1015/Disulfide bonds: #status predicted
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A,Realdues: 1.1533 «UDS)
A,Cross-references: UNIPROT:Q00546; GB:X64649; NID:g63613; PIDN:CAA45920.1; PID:g63614
A,Experimental source: brain
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F;656-696/Domain: LDL receptor YWTD-containing repeat homology <YW11>
F;697-739/Domain: LDL receptor YWTD-containing repeat homology <YW12>
F;747-782/Domain: EGF homology <EGS>
F;839-872/Domain: EGF homology <EGS>
F;878-914/Domain: EGF homology <EGS>
F;920-955/Domain: EGF homology <EGS>
F;970-1055/Domain: EGF homology <EGS>
F;971-1015/Domain: EGF homology <EGS>
F;971-1015/Domain: EGF homology <EGS>
F;071-1015/Domain: EGF homology <EGS>
F;071-1015/Domain: EGF homology <EGS>
F;071-1015/Domain: Lansamembrane #status predicted <TMM>
F;061-1035/Domain: intracellular #status predicted <TMM>
F;061-1133/Domain: intracellular #status predicted <TMM>
F;071-1133/Domain: intracellu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 41.1%; Score 46; DB 1; Length 1133; Best Local Similarity 37.5%; Pred. No. 1.9e+02; Matches 9; Conservative 3; Mismatches 6; Indels
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41.1%; Score 46; DB 1;
Best Local Similarity 27.8%; Pred. No. 2.1e+02;
Matches 10; Conservative 3; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the Safes Data Library, Angre 1999
A) Reservence number 180504
A) Reservence number 180504
A) Reservence number 180504
A) Reservence number 180504
A) Residuate 1995 and 180504
A) Ribborow, D. S. 1 Simpson, R. J.
A) Ribborow, R. J. Santh, J. A. Norliz, R. L. J. O'Hare, M. J. Rudland, P. S. J. Morrison, J. R. J. Ribborow, R. J. Santh, J. A. J. Morizz, R. L. J. O'Hare, M. J. Rudland, P. S. J. Morrison, J. R. J. Ribborow, R. J. Santh, J. A. J. Morizz, R. L. J. O'Hare, M. J. Rudland, P. S. J. Morrison, J. R. J. Ribborow, R. J. Santh, J. A. J. Worliz, R. L. J. O'Hare, M. J. Rudland, P. S. J. Morrison, J. R. J. Ribborow, R. J. Santh, J. A. J. Worlizz, R. L. J. O'Hare, M. J. Rudland, P. S. J. Morrison, J. R. J. Ribborow, R. J. Santh, J. A. J. Wollize 1990 and 1990
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Cispecies: Glycine max (soybean)
Cispecies: Glycine max (soybean)
Cispecies: Glycine max (soybean)
Cipate: 24 Apr-1944 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
Cipate: 24 Apr-1948 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
Cipate: All329 #segas-1918 #sequence No. 1918
A.Title: Molecular cloning and analysis of a gene coding for the Bowman-Birk protease inh A;Reference number: A92489, MUID:044264652; PMID:6086657
A;Contents: annotation
A;Note: the sequence has been revised in reference A92540
R;Hammond, R.W.; Poard, D.E.; Larkins, B.A.
A;Reference number: A92540
A;Reference number: A92540
A;Contents: erratum
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Ajaccession: A22636
Ajaclecule type: DNA
Ajaclecule type: DNA
Ajacss-references: UNIPROT: P01063; GB:K01967; NID:g169942; PIDN:AAA33952.1; PID:g169943
K) Gdani, S.; Kkenaka, T.
J. Biochem. 82, 1523-1531, 1977
AjTitle: Studies on soybean trypsin inhibitors. XI. Complete amino acid sequence of a soy
A,Reference number: A01302; MUID:78087480; PMID:599141
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C;Comment: This protein inhibits trypsin, elastase, and chymotrypsin. The site of interac C;Comment: This protein inhibits trypsin, elastase, and chymotrypsin. The site of interac C;Comment: This protein inhibitor.
C;Superfamily: Bowman-Birk proteinase inhibitor
C;Reywords: duplication; seed; serine proteinase inhibitor
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-103/Product: proteinase inhibitor (Bowman-Birk) C-II #status experimental <MAT>
F;28-103/Product: proteinase inhibitor repeat homology <BB1>
F;69-69/Domain: Bowman-Birk inhibitor repeat homology <BB2>
F;69-69/Domain: Bowman-Birk inhibitor repeat homology <BB2>
F;69-19/Domain: Bowman-Birk inhibitor repeat homology <BB2>
F;69-19/Domain: Bowman-Birk inhibitor repeat homology <BB2>
F;71-95,42-57,45-91,47-55,65-72,69-84,74-82/Disulfide bonds: #status predicted
F;76/Inhibitory site: Alg (trypsin) #status predicted
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Cispecies: Caenorhabditis elegans
Cispecies: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
Cispeciesion: T28789, L.
Submitted to the EMBL Data Library, May 1997
Alpescription: The sequence of C. elegans cosmid C41D11.
Alse Secription: T28784
Alse Session: T28784
Alse Session: T28784
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A;Introns: 62/3; 172/1; 403/3; 478/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C41D11.3
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                                                                                                                                                                                                                    hypothetical protein C41D11.3 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: UNIPROT:001972; EMBL:AF003740; PID
A,Experimental source: strain Bristol N2; clone C41D11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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Local Similarity 60.0%;
les 9; Conservative (
                                                                         62 RCACTRSMPGQCRCL 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecule type: protein
Residues: 28-103 <0DA>
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A;Gene: CESP:C41D11.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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A.Molecule type: mENA
A.Molecule type: mENA
A.Molecule type: mENA
A.Rosidues: 1-83 <00U>
A.Cross-references: UNIPROT: P01063; EMBL: M20732; NID: g169944; PIDN: AAA33953.1; PID: g1699
A.Cross-references of codons 8-13 and 14-27 are interchanged in the authors' translat R; Back, U.M.; Kim, S.I.
R; Back, U.M.; Kim, S.I.
submitted to the EMBL Data Library, October 1992
**.nearthion: Nucleotide sequence of a cDNA encoding the soybean Bowman-Birk proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Glycine max (soybean)
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 18-Aug-2000
C;Accession: JG2225
R;Baek, J.M.; Song, J.C.; Choi, Y.D.; Kim, S.I.
Biscal: Blotechnol, Blotchem. S8, 843-846, 1994
A;Title: Nucleoride sequence homology of cDNAs encoding soybean Bowman-Birk type protein A;Reference number: JG2224; MUID:94289861; PMID:7764974
                              C; Species: Glycine max (soybean)
C; Species: Glycine max (soybean)
C; Date i 02-Dec-1993 Hacquence revision 03-Nov-1995 #text_change 09-Jul-2004
C; Accession: S07405; S29608; S40113
R; Joudrier, P.E.; Foard, D.E.; Floener, L.A.; Larkins, B.A.
Plant Mol. Biol. 10, 35-42, 1987
A; Title: Isolation and sequence of CDNA encoding the soybean protease inhibitors PI IV
A; Reference number: S07408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1.83 <GTO.
A;Residues: BMBL:X76727; NID:g436413; PIDN:CAA54144.1; PID:g436414
A;Croser-references: EMBL:X76727; NID:g436413; PIDN:CAA54144.1; PID:g436414
C;Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
C;Keywords: serine proteinase inhibitor
F;22-48/Domain: Bowman-Birk inhibitor repeat homology <BBI>
F;49-74/Domain: Bowman-Birk inhibitor repeat homology <BBI2>
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.Comment: This protein regulates endogeneous proteinase during germination, stores sul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Start codon: GTT
;Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
;Reywords: duplication; seed; serine proteinase inhibitor
;1-18/Domain: signal sequence #status predicted <SIG>
;19-94/Product: Bowman-Birk proteinase isolnhibitor C-II #status predicted <MAT>
;33-59/Domain: Bowman-Birk inhibitor repeat homology <BBI2>
;60-85/Domain: Bowman-Birk inhibitor repeat homology <BBI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X68705; NID:g18567; PIDN:CAA48656.1; PID:g18568
R;Giordano, A.; Delledonne, M.; Fogher, C.; Marchetti, S.
submitted to the EMBL Data Library, December 1993
A;Description: Nucleotide sequence encoding a soybean C-II proteinase inhibitor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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proteinase inhibitor (Bowman-Birk) C-II - soybean
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Pred. No. 41;
0; Mismatches
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Best Local Similarity 60.0%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 RCACTRSMPGQCRCL 65
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Best Local Similarity 60.00
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A,Residues: 1-83 <BAE>
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Query Match
40.6%; Score 45.5; DB 2; Length 532;
Best Local Similarity 47.1%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 6; Indels
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3 CRCLCRRGVC---RCLC 16

298 CGCSCENGVCLPETCQC 314

엄

hypothetical protein SP5 - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C;Accession: S01186
R;Nishimatsu, S.I.; Murakami, K.; Mitsui, Y.; Ishida, N.
Nucleic Acids Res. 16, 11831-11832, 1988
A;Title: Mouse spleen derived cDNA clones containing per repeat sequence.
A;Reference number: S02186
A;Reference number: S02186
A;Accession: S02186
A;Cross-references: UNIPROT:P15974; EMBL:X12806; NID:g53649; PIDN:CAB42649.1; PID:g48037

Gaps Query Match 40.2%; Score 45; DB 2; Length 95; Best Local Similarity 52.6%; Pred. No. 51; Matches 10; Conservative 1; Mismatches 4; Indels

1 GVCRCLCRRGVCRC---LC 16

8 GVCLCVC-FSVCMCVHVLC 25

a

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probable dioxygenase beta chain YPO2492 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Species: Versinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 16-Aug-2004
C;Accession: AE0304
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. R;Parkhill, J. W.; Futherford, K.; Simmonds, M.; Skelton, J.; Stevens, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, R.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AE0304
A;Status: preliminary
A;Accession: AE0314
A;Accession: AE0

A;Gene: YPO2492 C;Superfamily: Phthalate dioxygenase reductase; cytochrome-b5 reductase homology; ferred C, Genetics:

Gaps ; Length 321; Query Match
40.2%; Score 45; DB 2; Length 321
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels

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5 CLCRRGVC 12

268 CLCREGIC 275

Search completed: October 26, 2004, 15:40:21 Job time : 25.5 secs

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177 VCQCLC---VCQCLC 188
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Q6ZMP3
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 Q6ZMP3
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982271 macaca mula

982271 macaca mula

982271 macaca mula

982812 mus musculu

886h20 mus musculu

Aah61079 mus musculu

094k2 mus musculu

01828 caenorhabdi

02182 caenorhabdi

021821 caenorhabdi

03122 homo sapien

06292 homo sapien

06292 homo sapien

07046 anopheles

07046 anopheles

07182 coturnix co

081mid drosophila

071820 coturnix co

06185 homo sapien

06185 homo sapien

06185 homo sapien

06185 homo sapien

06185 homo sapien
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09w0a0 drosophila
07prp5 anopheles g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                            , Search time 128.5 Seconds (without alignments) 80.597 Million cell updates/sec
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                               1825181 segs, 575374646 residues
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Maximum Match 100%
Listing first 45 summaries
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BAC87611
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Q7YWV7
Q81HD6
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Q81HJ2
Q81HJ2
O7SXV0
O57352
O7SXV0
O57352
AAHG3685
                                                                  OM protein - protein search, using sw model
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BAD18682
P82271
Q9D912
Q6P8T4
Q8CH20
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Q18238
Q122048
Q922041
Q17641
Q949G1
Q90123
Q60123
Q6RY99
AAR24072
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Q9W0A0
Q7PRP5
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112
1 GVCRCLCRRGVCRCLCRR 18
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Gapop 10.0 , Gapext
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length: 2000000000
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Perfect score:
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Maximum DB
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RECUENCE FROM N.A.

RECUENCE FROM N.A.

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TISSUE=Tongue; N. Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,

RA Tanigami A., Fujiwara T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,

RA Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,

RA Isno Y., Kawai-Hio Y., Satio K., Nishikawa T., Kimura K.,

RA Sugiyama A., Marsuwa K., Ranehori K., Takahashi-Fujii A., Oshima A.,

RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,

RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,

RA Sugiyama A., Rawakami B., Suzuki Y., Sugano S., Nagahari K.,

RED Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

BR Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

BR GO: GO:0016301; F.kinase activity; IEA.

DR GO: GO:016301; F.kinase activity; IEA.

DR FUNIS; PRO0008; DAGPBDOMAIN.

DR FAMN: SM00109; C1; 1.

BRART; SM0109; C1; 1.

PR PRONZIE; PSS0081; DAG-PE_BIND_DOM_2; 1.
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                      086502 mus musculu

067599 mus musculu

080000 mus musculu

080000 mus musculu

080654 homo sapien

060002 brachydanio
                                                                                                  Q8bpc0 mus musculu
Q9h654 homo sapien
Q6qp2 brachydanio
Q9xvx3 caenorhabdi
Q8irl0 drosophila
Q8iq18 drosophila
Aan10358 drosophil
  trypanosoma
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI TaxID=9606;
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Q8bw14 mus musculu
Q8n962 homo sapien
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BAD18682;
12-MAY-2004 (TrEMBLrel. 27, Created)
12-MAY-2004 (TrEMBLrel. 27, Last sequence update)
12-MAY-2004 (TrEMBLrel. 27, Last annotation update)
12-MAY-2004 (TrEMBLrel. 27, Last annotation update)
Kinase C, delta type (EC 2.7.1.-).
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-UTL-2004 (TrEMBLrel. 27, Created)
05-UTL-2004 (TrEMBLrel. 27, Last sequence update)
05-UTL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FLJ16784.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7%; Pred. No. 3.4;
Matches 10; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
07YUU2
08C9N2
08C9N2
08C9N2
08BPC0
08BPC0
08GP2
09C9VX3
081LL0
081018
AAN10358
0PR44
08N9624
08N9624
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EMBL; AF184156; AAF07923.1; -.
                                                                                                                                                                                                                                                                                  8189 MW;
                                                                                                                                                                                                                                                                                                                                  53.6%;
                                                                                                                                                                                                                                                                                                                                                         83.3%;
                                                                                                                                                                                                                                                                                                                                                    Local Similarity 83.3
                                                                                                                                                                                                                                                                                                                                                                                                                             4 RCLCRRGVCRCL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 RCLCRRGVCOLL 76
                                                                                                                                                                 20
                                                                                                                                                                                  64
73
76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                     76 AA;
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                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9D9I2
Q9D9I2;
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                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                          PROPEP
                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Q9D912
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  STITIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             유
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                                                                                                                                     Tanigami A. Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F., Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamateu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamaehita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; "NEDO human cDNA sequencing project."; Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhao C., Nguyen T., Lehrer R.I.;

"cDNA cloning of three alpha-defensins and three demidefensins from
rebsus monkey bone marrow."

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

-! FUNCTION. Microbloidal activity against Cram-positive bacteria

S. aureus and L. monocycogenes, Gram-negative bacteria S. typhimurium
and E.coli ML35 and fungi C.albicans and C.neoformans in vitro.

-! SUBNITI: Heterodimer of subunit A and subunit B linked by a
disulfid bond at position 66 forming a cyclic RTD-1.

-! TISSUE SPECIFICITY: Bone marrow; promyelocytes, myelocytes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., SEQUENCE OF 65-73, AND MASS SPECTROMETRY.
TISSUE=Bone marrow, and Leukocyte;
MEDLINE=99453140; PubMed=10521339;
MEDLINE=99453140; PubMed=10521339;
Ouellette A.J., Yuan J., Osapay G., Osapay K., Tran D., Miller C.J.,
"A Cyclic Antimicrobial Peptide Produced in Primate Leukocytes by the Ligation of Two Truncated alpha-Defensins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       early during granulocytte myelopoiesis.
-!- MASS SPECTROMETRY: MW=2082.0; METHOD=MALDI.
-!- MISCELLANEOUS: The determined pI of this protein is greater than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mature neutrophils and monocytes.
-!- DEVELOPMENTAL STAGE: Expression and peptide accumulation starts
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    243 AA; 27566 MW; 23D41825EB9F782D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Theta defensin-1, subunit B precursor (RTD-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 60.5; DB 2;
Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 VCQCLC---VCQCLC 188
                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AK131548; BAD18682.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VCRCLCRRGVCRCLC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 66.7 es 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cercopithecinae; Macaca.
                                                                                               SEQUENCE FROM N.A. TISSUE=Tongue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9544;
                                Mammalia, Euther
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                Kinase.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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P82271
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-1- SIMILARITY: Belongs to the corticostatin/defensin family. EMBL; AF191101; AAF04390.1; -. EMBL; AF191103; AAF04392.1; -.

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SEQUENCE FROM N.A.
STRAIN=C57BL/G07 IISSUE=Testis;
MEDLINE=20499374; PubMed=1104159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itch M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the RIKEN Genome Exploration Research Group Phase I & II Team; the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 12, Last squence update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:1700065105 product:hypothetical Cysteine-rich region
containing protein, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                        Score 60; DB 2; Length 76; Pred. No. 1.4;
                                                                                                                                              THETA DEFENSIN-1, SUBUNIT B. REMOVED IN MATURE FORM.
                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                    F0B754466156071E CRC64;
                   IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CS7BL/65; TISSUE=Testis;
MEDLINE-99279253; PubMed-10349636;
Carnhnoi P., Hayashizaki Y.
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
PIR; B59089; B59089.
GO; GO:0050812; P:defense response to fungi;
GO; GO:0006805; P:xenobiotic metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 AA
                                                                                                                                                                                                                                                                               1; Mismatches
                                                   InterPro; IPR002366; Defensin propep.
Pfam, PP00879; Defensin propep; 1.
Antibiotic; Defensin; Fungicide; Signal.
                                                                                                             POTENTIAL.
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STRAIN=CSTRIA(4):
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM CONSORTIUM;
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STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=20530913; PubMed=11076861;
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STRAIN=CS7BL/6J; TISSUE=Testis;
The FANTOM Consortium,
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and mouse cDNA sequences.";
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Matches
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Alusner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Antschul S. B., Boraldo M.F., Casavant T.L., Scheetz T.E.,

Braheton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toobhyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzarne P.H.,

Richards S., Worley K.C., File S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., File S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Shevchenke Y., Bouffard G.G.,

Mhiting M., Madan A., Young A., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

STRAIN-CSTBL/6J; IISSUB-Testis;
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
A dachi J., Aizawa K., Akahira S., Rukuda S., Fukunishi Y., Furuno M.,
A darawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
A mangaki T., Hara A., Hayatsu N., Hiramcto K., Hiracka T., Hori F.,
A mani J., Kolima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata W., Shibata Y., Shinagawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramateu M., Hayashizaki Y.,
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shono H., Akiyama T., Nishi K., Kitaunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yaliwake S., Inoue K., Togawa Y., Izawa M., Chara E., Matshika M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matshiki M., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., Sequencing integrated sequence analysis (RISA) system-384-format sequencers.";
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53.6%; Score 60; DB 2; Length 168; 56.2%; Pred. No. 2.9; tive 0; Mismatches 7; Indels
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SEQUENCE 168 AA; 18931 MW; 7A2BD279612A5E94 CRC64;
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Last annotation update)
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Mus musculus (Mouse).
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TISSUE=Testis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH61079;
14-ARR-2004 (TEMBLrel. 27, Created)
14-ARR-2004 (TEMBLrel. 27, Last sequence update)
14-ARR-2004 (TEMBLrel. 27, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinse, Mus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                     Length 168;
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MGD; MGI.1913992; 4931420D14Rik. SEQUENCE 168 AA; 18957 WW; 8F30D3D27B9BF595 CRC64;
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                                                                                                      Strausberg R.; Submitted (MOV-2003) to the EMBL/GenBank/DDBJ databases. EMBL; ECG1079; AAHG1079.1; -. Hypothetical protein. SEQUENCE 168 AA; 18947 MW; BOOFD3D27B9BF768 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8CH20;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
sasic protein CKTIR3.
Name=4931420D148ik; Synonyms=Cktlr3;
Mus musculus (Mouse).
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Pred. No. 5.1;
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56.2%;
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Best Local Similarity 56.2"
Best Local 9, Conservative
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les 9; Conservative
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., R.chards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vilalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez M., Mihting M., Madan A., Young A.C., Shevchenko Y., Boiffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E., Goneration and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
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Nature 420:563-573(2002).
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-CT-2002 (TrEMBLrel. 22, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4931420D14 product:hypothetical Cysteine-rich region
containing protein, full insert sequence.
Name=4931420D14Rik;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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STRAIN=CS7BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM CONSOLTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
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Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC061079; AAH61079.1; -.
Hypothetical protein.
SEQUENCE 168 AA; 18947 MW; B00FD3D27B9BF768 CRC64;
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MEDLINE=99279253; Pubmed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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STRAIN-C57BL/6J; TISSUE=Testis;
MEDLINE=20499374; PubMed=11042159;
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STRAIN-EC5/BL/6J; TISSUE=Testis;
STRAIN-EFANTOM CONSOLIUM,
the RIKEN Genome Exploration Res
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Best Local Similarity 56.22
Best Local 9; Conservative
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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R. Embl. AKOL6467; BAB30253.1; S.
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; Muzamatication of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                    SEQUENCE FROM N.A.
SIGUENCE FROM N.A.
SIGUENCE FROM N.A.
X MEDLINE-20530013; Pubmed-11076861;
A MEDLINE-20530013; Pubmed-11076861;
A Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunco H., Itoh M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunra S., Rawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., Rayan T., Ozawa K., Tanaka T., Matsunra S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Rayan S., Rayal J., Genome Res. 10:1757-1771(2000).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 26, Last annotation update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
0RFNames=C27A2.5;
Caenorhabditis elegans.
Elbaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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SEOUENCE 173 AA: 19581 MW; 147B6F155AC29FDF CRC64;
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"Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).

SEQUENCE FROM N.A. STRAIN=Bristol N2; Nhan M.;

MEDLINE=99069613; PubMed=9851916;

Wilson R.;

SEQUENCE FROM N.A.

NCBI_TaxID=6239;

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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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STRAIN=Bristol N2;
Waterston R.,
Submitteed (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; U5584; AAK68158.1;
RMSPP; P10969; IX7V.
RMSPP; P10969; IX7V.
RMSPP; P10969; IX7V.
RMSPP; P1096081; Defensin_alpha.
InterPro; IPR006081; Defensin_alpha.
RMSPPP: IPR006081; Defensin_alpha.
RMSPPP: IPR006209; EGF_11ke.
RMSPROSITE; P800199; JAF48; FEREDOXIN; UNGNOWN_1.
RMSPROSITE; P8001029; DEFENSIN; UNGNOWN_1.
RMSPROSITE; P801029; DEFENSIN; UNGNOWN_1.
RMSPROSITE; P801029; UFFENSIN; UNGNOWN_1.
RMSPROSITE; P801029; WFFEZ_1; UNGNOWN_1.
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                     Query Match 50.9%; Score 57; DB 2; Length 164; Best Local Similarity 55.6%; Pred. No. 6.6; Matches 10; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anderson K., Chissoe S.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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017641,
01-NOV-1996 (TEMBLEEL: 01, Created)
01-OCT-2001 (TEMBLEEL: 18, Last sequence update)
01-MAR-2004 (TEMBLEEL: 26, Last annotation update)
Hypothetical protein C04G6.7.
                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypotheitcal protein CO4G6.10.
ORFNames=CO4G6.10;
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STRAIN-Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                  WormPep; C27A2.5; CE04105.

R GO; GO: 0005576; C: extracellular; IEA.

GO; GO: 0005576; C: extracellular; IEA.

GO; GO: 0005613; P: defense response; IEA.

R GO; GO: 0005613; P: response to pest/pathogen/parasite; IEA.

InterPro; IPR001450; 4Fe4S_ferredoxin.

InterPro; IPR00107; VMF.

PROSITE; PS001289; 4Fe4S_FERREDOXIN; UNKNOWN_1.

PROSITE; PS01208; VMFC_1; UNKNOWN_1.

PROSITE; PS01208; VMFC_1; UNKNOWN_1.

PROSITE; PS01208; VMFC_1; UNKNOWN_1.

RPOSITE; PS01208; VMFC_1; UNKNOWN_1.
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55.6%; Pred. No. 5.6;
cive 0; Mismatches 8; Indels
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Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; 52649; CAA91301.1; -.
PIR; T24272; T24272.
HSSP; P10968; 2CWG.
                                              SEQUENCE FROM N.A.
STRANTH-BATISTO N2;
WATCHING (NOV-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, 108766; AXX31463.1;
PIR; T15621; T15651.
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAX-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein T01B7.8.
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InterPro; IPRO01450, 4Fe4S, ferredoxin.
InterPro; IPRO06081; Defensin_alpha.
InterPro; IPRO06081; Defensin_alpha.
InterPro; IPRO01007; WWF.C.
PROSITE; PS001289; 4FF4S, FERREDOXIN, UNKNOWN_1.
PROSITE; PS001289; DEFENSIN, UNKNOWN_1.
PROSITE; PS01208; WWF.C.
Hypothetical protein.
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STRAIN-Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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nes 10; Conservative
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Q22048;
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274 AA; 28657 MW; AB547D9BD5470AE1 CRC64;
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SEQUENCE FROM N.A.
STRAIN=U1102;
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Caenorhabditis elegans.
Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; USSB4; AAK6161.1;
WormPep; C04G6.7; CE27652.
MormPep; C04G6.7; CE27652.
InterPro; IPR001450; 4F645. ferredoxin.
R InterPro; IPR006209; EGF_like.
R InterPro; IPR006209; EGF_like.
R InterPro; IPR006209; EGF_like.
R PROSITE; PS00199; 4F645. FERREDOXIN; UNKNOWN_1.
R PROSITE; PS00129; FERREDOXIN; UNKNOWN_1.
R PROSITE; PS001209; WFC_l; UNKNOWN_1.
R PROSITE; PS01208; WFC_l; UNKNOWN_1.
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Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
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EMBL, AJ307662; CAC39030.1; -.
Gramene; Q949G1; -.
Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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STRAIN=U1102;
MEDLINE=90080132; PubMed=2152817;
Lawrence G.L., Chee M., Craxton M.A., Gompels U.A., Honess R.W.,
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TISSUB-Liver;
Zhang S., Duyang S., Luo L., Wei H., Zhou G.,
Zhang Y., Liu M., He F.;
Zhang Y., Liu M., He F.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF11848; AF16687.1;
SEQUENCE 190 AA; Z1480 MW; 4B8104A29AA33844 CRC64;
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  Score 57; DB 2; Length 274;
Pred. No. 10;
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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Last sequence update)
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/ Match 50.9%; Score 57; DB Local Similarity 60.0%; Pred. No. 10; les 9; Conservative 0; Mismatches
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MEDLINE=90112641; Pubmed=2153237;
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01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2002 (TrEMBLrel. 22,
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Thomson B.J., Honess R.W.;
"The right end of the unique region of the genome of human herpesvirus 6 Ullo2 contains a candidate immediate early gene enhancer and a homologue of the human cytomegalovirus US22 gene family.";
                                                                                                        STRAIN=U1102;
MEDLINE=91333007; PubMed=1651403;
Teo 1.A., Griffin B.E., Jones M.D.;
"Characterization of the DNA polymerase gene of human herpesvirus 6.";
J. Virol. 65:4670-4680(1991).
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MEDLINE=91374590; PubMed=1654446;
MEDLINE=91374590; PubMed=1654466;
Martin M.E.D., Nicholas J., Thomson B.J., Newman C., Honess R.W.;
Mactin M.E.D., a transactivating function mapping to the putative immediate-early locus of human herpesvirus 6.";
J. Virol. 65:5381-5390(1991).
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MEDLINE=22148942; PubMed=1310766;
Geng Y., Chandran B., Josephs S.F., Wood C.;
"Identification and characterization of a human herpesvirus 6 gene segment that trans activates the human immunodeficiency virus type 1
      Thomson B.J., Efstathiou S., Honess R.W.;
"Acquisition of the human adeno-associated virus type-2 rep gene by human herpesvirus type-6.";
Nature 351:78-80(1991).
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MEDLINE=92266671; PubMed=1374813;
Neipel F., Ellinger K., Fleckenstein B.;
"Gene for the major antigenic structural protein (p100) of human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The glycoprotein B homologue of human herpesvirus 6.";
J. Gen. Virol. 74:495-500(1993).
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MEDLINE-92333249; PubMed-1321206;
MEDLINE=91226542; PubMed=1851252;
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MEDLINE-93187613; PubMed-8383182;
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Chandran B.;
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MEDLINE=93331710; PubMed=7687803;
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MEDLINE=94025598; PubMed=8212582;
MEDLINE=93091236; PubMed=1333836;
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MEDLINE=94167865; PubMed=8122364;
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Oncogene 9:1167-1175(1994)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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GO, GO:0004872; F:receptor activity; IEA.
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InterPro; IPR001309; Ribosomal S14.
InterPro; IPR0019091; Transmem 4.
PPG0355; Tetraspannin; I.
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tive 1; Mismatches 4;
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Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,
Sugiyama T., Irie R., Otsuki T., Sato H., Wakanatsu A., Ishii S.,
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EMBL; AK128797; BAC87611.1; -
EMBL; AK128797; BAC87611.1; -
ERSEQUENCE 201 AA, 20938 MW; 3408F8B817AA0500 CRC64;
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                      STRAIN-Wistar; TISSUE-Hippocampus; Andriamampadry C., Taleb O., Viry S., Muller C., Humbert J.P., Andriamampadry C., Taleb O., Viry S., Muller C., Humbert J.P., "Clouding and characterization of a rat brain receptor that binds the endogenous neuromodulator gamma-hydroxybutyrate."; FASEB J. 0.0-0(2004).

EMBL; AY485933; AAR24072.1; -.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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2; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          512 AA; 56146 MW; 44DD12B937C40D60 CRC64;
02-WAR-2004 (TrEMBLrel. 27, Created)
02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q6ZQS2;
05-UIL-2004 (TrEMBLrel. 27, Created)
05-UIL-2004 (TrEMBLrel. 27, Last sequence update)
05-UIL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FLJ45585.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49.6%; Score 55.5; DB 2;
64.7%; Pred. No. 28;
ive 1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                             Gamma-hydroxybutyrate receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       385 VCVCVCVR-VCLCLCVR 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VCRCLCRRGVCRCLCRR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Query Match
Best Local Similarity 64.79,
Conservative
Conservative
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Best Local Similarity 53...
Best Acas 8; Conservative
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                                                                                                                      Rattus norvegicus (Rat).
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RESULT 19 BAC87611

385 VCVCVCVR-VCLCLCVR 400

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Eukaryota, Metazoa; Nematoda, Chromadorea; Rhabditida, Rhabditoidea;
Rhabditidae, Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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Stapleton M., Brookstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
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Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Brooptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kershaw J.K.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; Z81579; CAE17915-1; --
InterPro; IPRO06209; EGF like.
InterPro; IPRO01007; VWFC.
InterPro; IPRO01007; VWFC.
INTERPRO; PROSITE; PS00129; GGF 1; UNKNOWN 1.
PROSITE; PS01208; VWPC-1; UNKNOWN 1.
PROSITE; PS01208; VWPC-1; UNKNOWN 1.
PHypothetical protein.
SEQUENCE 212 AA; 22857 WW; 22F62CE4073CCA4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.2%; Score 54; DB 2; Length 905; ilarity 52.9%; Pred. No. 70; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.2%; Score 54; DB 2; Length 212; 56.2%; Pred. No. 20; 1:ve 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MCV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BT001299; ABN71054-1; --
FlyBase; FBGN0051029; CG31029.
SEQUENCE 905 AA; 102573 MW; 301303CE74E9D29E CRC64;
01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-WAR-2004 (TrEMBLrel. 26, Last annotation update) Hypothetical protein R13H4.8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       905 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel, 23, Created)
01-MAR-2003 (TrEMBLrel, 23, Last seq
01-MAR-2004 (TrEMBLrel, 26, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                  STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AT12234p.
Name=CG2164; ORFNames=CG31029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GVCRCLCRRGVCRCLCR 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 CGCCCCRPRCCCCCRR 99
                                                                                                                                                                                                                                                                                                                                                                 investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 56.2 Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                         Name=R13H4.8;
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=Bristol N2;
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                                                                                                                                                                                                                                          SEQUENCE
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0
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Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,
Kanehori K., Ishibashi T., Chiba S., Ono Y., Hotuta T., Watanabe M.,
Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatu A., Ishii S.,
Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
Wagatuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
"NEDO human cDNA sequencing project.";
"NEDO human cDNA sequencing project.";
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AK128797; BACG7611.1;
SEQUENCE 201 AA; 20938 MW; 3408FBE817AA0500 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
NCBI_TaxID=180454;
                                                          02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
CDNA FL/15585 [is, clone BRTHA3013882.
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primata; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anotheles Genome Sequencing Consortium;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL; AAAB01000199; EAA45966.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h similarity 53.3%; Pred. No. 14; 8; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212 AA; 23844 MW; 28984CAECB21D496 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ENSANGE00000024926 (Fragment).
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                  201 AA
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                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        || |:| || |:| |:| |:| se vclcvclvsvclcvc 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VCRCLCRRGVCRCLC 16
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nes 9; Conservative
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                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                  BAC87611
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Matches
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Q7PDW6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAMEDLINE-20196006; PubMed=10731132;

RAMAMA M. CeLnikers S.E., Hip P.W., Hoskins R.A., Galle R.F.,

RAMAMA M.D., CeLnikers S.E., Hip P.W., Hoskins R.A., Galle R.F.,

RAMAMA M.D., CeLnikers S.E., Richards S., Ashburner M., Henderson S.N.,

RAMAMA M. Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RAMAMA M. L. Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RAMAMA M. L. Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RAMA Abril J.F., Agbayani A., An H.J., Andrews-Fammicoch C., Baldwin D.,

Ballew R.M., Benos P.V., Berman B.P., Bandari D., Bolshakov S.,

RAMA Borkova D. Botchan M.R., Bouck J., Brokstein P., Brottler P.,

RAMA Borkova D.A., Buller H., Cadleu E., Center A., Chandra I.,

RAMA BORNON K.J. Doup L.B., Downes M., Dugan-Rocha S., Punkov S.,

RAMA Durbin K.J., Evangelista C.C., Ferraz C., Perriera S., Plaischman W.,

RAMA Gabriellan A.B., Gary N.S., Gelbart W., Idasser K.,

RAMA Gong F., Gorrell J.H., Guller M., Moy M., M.,

RAMA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RAMA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RAMAMA M., Murphy B., Maryl S., Miller M., Moy M.,

RAMAMA M., Murphy B., Murphy L., Maryl S., Morberson D.,

RAMAMA M., Murphy B., Murphy L., Maryl S., Morberson D.,

RAMAMA M., Moy M., Murphy B., Murphy L., Marzh J., Moshrefi A.,

RAMAMA M., Palush R., Ralander R., Woller W., Shigh H.,

RAMAMA M., Palush R., Rappeton M., Stupski M. P., Smith T.,

Razzolo M., Pitchan G.S., Pan S., Pollard J., Worles D.,

RAMAMA M., Murphy B., Murphy L., Marzh J., Wasser M.G.,

RAMAMA M., Moy M., Murphy B., Murphy L., Marzh J., Moshrefi A.,

RAMAMA M., Moy M., Murphy B., Murphy L., Marzh J., Wasser M.G.,

RAMAMA M., Radama R.S., Pan S., Pollard J., Wasser M.G.,

Razzolo M., Pitchan G.S., Pan S., Pollard J., Wasser M.G.,

Ray Spier E., Spradling A.C., Stapleton M., Stupski M. P., Smith H.O.,

Ray Shiera R., Zhong R., Rabing G., Zhong R., Smith H.O.,

Ray Shiera R., Shanda R., Rabing G., Zhong S., Yao Q.A., Ye J.,

Ray Shiera R., San, Woodager,
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                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                               905 AA
                                                                                                                                                                                    Created)
                                                                                                                               PRT.;
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MEDLINE=22426070; PubMed=12537573;
  728 GFAPCTCRRPVASCFCR 744
                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                             CG31029-PA.
ORFNames=CG31029;
                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7227;
                                                                                                                                                                                  01-MAR-2003
01-MAR-2003
                                                                                                                                  Q8IMJ2
                                                                                RESULT 23
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STAIN-AB; TISSUE-Whole body;

STRAIN-AB; TISSUE-Whole body;

SX STRAIN-AB; TISSUE-Whole body;

SX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

SA Altschul S.E., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.E., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.E., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

By Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

By Explecton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carnindi P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P. H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hllyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mitting M., Madan A., Young A., Rockingues S., Sanchez A.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Fistse E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E., The Company of the Drosophila melanogaster euchromatin: "The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Misra S., Crosby M.A., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Fradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Bukaryota; Metazoa; Chordata; Craniata; Vortebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.

NCBI_TaxID=7955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lewis S.E.;
"Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.2%; Score 54; DB 2; Length 905; 52.9%; Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59471B320E041C20 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
101-OLT-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein zgc:63759.
Name=zgc:63759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
                                                                                                                                                                                                     Genome Biol. 3: RESEARCH0084-RESEARCH0084 (2002).
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SEQUENCE 905 AA; 102461 MW;
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                                                                                                                                                                genomics perspective.";
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Best Local Similarity
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Rodziguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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Bichmann A., Corbel C., Jaffredo T., Breant V., Joukov V., Kumar V.,
Alitalo K., Le Douarin N.M.;
"Avian VEGF-C: cloning, embryonic expression pattern and stimulation
of the differentiation of VEGFR2 expressing endothelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Potential.
vascular endothelial growth factor C.
; 099BFCC79151BF2B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                    Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC055236; AAH55236.1; -.
InterPro; IPR002172; LDL receptor.A.
Pfam; PF00057; Ldl recept.a; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 protein. _ 379 AA; 40591 MW; D763CB41A9F752C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                057352;
01-UJN-1998 (TrEMBLrel. 06, Created)
01-UJN-1998 (TrEMBLrel. 06, Last sequence update)
01-UJN-2003 (TrEMBLrel. 24, Last annotation update)
Vascular endothelial growth factor C precursor.
                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         418 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 47.8%; Score 53.5; D
Local Similarity 45.5%; Pred. No. 38;
hes 10; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    345 VCLCVTEVLSDPCCRGVCVCVC 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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PROSITE; PSS0278; PDGF 2; 1.
Growth factor; Mitogen; Signal.
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                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=AB; IISSUE=Whole body;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                          SMART, SM00192, LDLa; 6. PROSITE; PS01209; LDLRA_1; 6. PROSITE; PS01209; LDLRA_2; 6. Hypothetical protein.
SEQUENCE 379 AA; 40591 MW;
                                                                                                              and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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418 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=VEGF-C;
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Matches
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057352
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Kausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
Attausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buttow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Bitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Rapleton M.J., Usdin T.B., Donaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Galbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROW N.A., AND SEQUENCE OF 103-120.
MEDLINES-96179224; PubMed=8647204;
MEDLINES-96179224; PubMed=8647204;
Joukov V., Pajusola K., Kaippainen A., Chilov D., Lahtinen I., Kukk E., Saksela O., Kalkkinen N., Alitalo K.;
Anvel vascular endothelial growth factor, VEGF-C, is a ligand for the Flt4 (VEGFR-3) and KDR (VEGFR-2) receptor tyrosine kinases.";
EMBO J. 15:290-298(1996).
                                                                                                                                                                                                                                                                       01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2004 (Rel. 45, Last annotation update)
vascular endothelial growth factor C precursor (VEGF-C) (Vascular endothelial growth factor protein) (VRP) (Flt4 ligand) (Flt4-
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96203094; PubMed=8612600;
Joukov V., Pajusola K., Kaipainen A., Chilov D., Lahtinen I., Kukk
Sakkela O., Kalkkinen N., Alitalo K.;
EMBO J. 15:1751-1751(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and
                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                          15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE=97388482; PubMed=9247316; Fitz L.J., Norris J.C., Towler P., Long A., Burgess P., Greco Wang J., Gassaway R., Nickbarg E., Kovacic S., Ciarletta A., Giannotti J., Weinerty H., Zollner R., Beier D.R., Leak L.V., Turner K.J., Wood C.R.; "Characterization of murine Flt4 ligand/VEGF-C.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Glial tumor;
MEDLINE-96312526; PubMed-8700872;
Lee J., Gray A., Yuan J., Luoh S.-M., Avraham H., Wood W.I.;
"Vascular endothelial growth factor-related protein: a ligand
specific activator of the tyrosine kinase receptor Flt4.";
Proc. Natl. Acad. Sci. U.S.A. 93:1988-1992(1996)
Score 53.5; DB 2; Length 418;
Pred. No. 41;
6; Mismatches 1; Indels 15
                                                                                                                                                                                                                                     419 AA.
                                                                                                             290 COCVCKGGVRPISCGPHKELDRASCQCMCK 319
                                                                                  3 CRCLCRRGV-----CRCLCR 17
47.8%;
Query Match
Best Local Similarity 26.7
Matches 8; Conservative
                                                                                                                                                                                                                                     STANDARD;
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P49767
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3 CRCLCRRGV----
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                                                        32
112
228
280
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CARBOHYD
CARBOHYD
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DOMAIN
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REPEAT
REPEAT
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Q6FH59
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                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Barra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Generation and initial analysis of more than 15,000 full-length human
                                                                                               SEQUENCE OF 32-41; 112-121 AND 228-233, AND MUTAGENESIS OF ARG-227. MEDLINE=97377029; PubMed=2233800; Joukov V., Sorsa T., Kumar V., Jeltsch M., Claesson-Welsh L., Cao Y., Saksala O., Kalkkinen N., Alitalo K.; "Proteolytic processing regulates receptor specificity and activity of "Proteolytic processing regulates"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM, 601528; -...
GO; GO:0007315; P:lymph gland development; TAS.
GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
GO; GO:0007165; P:signal transduction; TAS.
GO; GO:0007165; P:signal transduction; TAS.
GO; GO:0007165; P:substrate-bound cell migration; TAS.
InterPro; IPR0024103; CXCXC_repeat.
InterPro; IPR004103; GF_CYSKnot.
InterPro; IPR000072; P_Growth_factor.
Pfam; PF03128; CXCXC; 5.
Pfam; PF03128; CXCXC; 5.
Pfam; PF03128; CXCXC; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -:- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0438; GFCYSKNOT.
ProDom; PD001629; PD growth_factor; 1.
PROSITE; PS00249; PDGF 1; 1.
PROSITE; PS50278; PDGF 2; 1.
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EMBL; U43142; AAA85214.1; -
EMBL; U58111; AAB02999.1; -
EMBL; BC035212; AA435212.1; -
PIR; S69207; S69207.
FISP; P49763; 1FZV.
Genew; HGNC.112682; VEGFC.
MIM; 601528; -
                                                                                                                                                                                    EMBO J. 16:3898-3911(1997).
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By similarity.

By similarity.

By similarity.

Interchain (By similarity).

Interchain (By similarity).

N-linked (GlcNAc. .) (Potential).

N-linked (GlcNAc. .) (Potential).

N-linked (GlcNAc. .) (Potential).

R-S: No proteolytic processing and lower effect on VEGRP-2 and VEGRP-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                         Or 102.
Vascular endothelial growth factor C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Angiogenesis; Cleavage on pair of basic residues;
Direct protein sequencing; Glycoprotein; Growth factor; Mitogen;
Multigene family; Repeat; Signal.
SIGNAL
PROPEP 32 111
                                                                                                                                                                  4 X 16 AA REPEATS OF C-X(10)-C-X-C-X(1,3)-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S., Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S., Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W., Korn B., Zuo D., Hu Y., LaBaer J.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
-!-SIMILARITY: Belongs to the PDGF/VEGF growth factor family. EMBL; CR541897; CAG46695.1; -.
InterPro; IPR004163; CXCXC, repeat.
InterPro; IPR002400; GF_CYSKnot.
InterPro; IPR000772; PD_growth_factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 47.8%; Score 53.5; DB 2; Length 419; Local Similarity 26.7%; Pred. No. 41; loss 8; Conservative 6; Mismatches 1; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46943 MW; 9F598703C13E1B55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 53.5; DB Pred. No. 41; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           291 CQCVCRAGLRPASCGPHKELDRNSCQCVCK 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             419 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- CRCLCR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -- CRCLCR 17
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Pfam; PF03128; CXCXC; 4.
PRINTS; PR0041; PDGF; 1.
ProDom; PD001629; PD growth_factor; 1.
SMART; SM00141; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46883 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 CRCLCRRGV-----
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26.7%;
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PROSITE; PS50278; PDGF 2; 1.
Growth factor; Mitogen.
SEQUENCE 419 AA; 46943 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 26....
Best Local Similarity 26....
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                                                                                                           111
227
419
362
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|:|:|| |: |291 CQCVCRAGLRPASCGPHKELDRNSCQCVCK 320

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**X ** MEDLINE=22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Sthuler G.D., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altacher R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C., Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C., Brohas S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Broas S.J., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H., Richards S., Worley K.C., Hale S., Gardan A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Anden A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Anderseley R.W., Touchman J.W., Green E.D., Dickson M.C., Stalska U., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Schnerch A., Schein
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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PubMed=14702039;
Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 41;
6; Mismatches 1; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC063685; AAH65685.1; -.
SEQUENCE 419 AA; 46883 MW; 9F598719DB3E014F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-CCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ12547.
Homo sapiens (Human).
                                                                            02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Vascular endothelial growth factor C preproprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                            PRT;
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26.7%;
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Best Local Similarity 26./*
Best Local 8; Conservative
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                         PRELIMINARY;
                                                                                                                                                                                        Homo sapiens (Human)
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TISSUE=Bladder;
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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NCBI_TaxID=9606;
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                               AAH63685
                                                     AAH63685
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AAH63685
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Gaps

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RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K., RA Wurakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A., RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., RA Takahashi M., Kanda K., Yoki T., Furuya T., Kikkawa E., Omura Y., RA Takahashi T., Yamashita H., Murakawa K., Fujimori K., Raniomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K., RA Tanai H., Kimata M., Watanabe M., Hiracka S., Chiba Y., Ishida S., Ranehori K., Takidashi-Fujii A., Hara H., Tanase T., Nomura Y., RA Kanehori K., Takidashi-Fujii A., Hara H., Tanase T., Nomura Y., RA Kanehori K., Takinashi-Fujii A., Hara H., Tanase T., Nomura Y., RA Kanashina Y., Matsunawa H., Ichihara T., Shiohata N., Sano S., Aobikawa Y., Matsunawa H., Satoh N., Takami S., Terakami Y., Rawakami S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Rawabata A., Hikiji T., Kobatake N., Takemoto M., Rawakami T., Okama M., Tashiro M., Chunara T., Shiohata A., Fujiwara T., Matsumura K., Nakajima Y., Matanabe K., Kumagai A., Itakura S., Fukuzumi Y., Rawabata A., Hikiji T., Kobatake N., Inagaki H., Natanabe T., Sugano S., Ttoh T., Shigeta K., Senba T., Rayashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Sasaki M., Rayashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Sasaki M., Rayashi K., Yada T., Satoh T., Shitani Y., Namashita R., Nakamura K., Nakamura Y., Ohara O., Isogai T., Sagano S., Rombari R., Pulakami T., Oyama M., Hata H., Watanabe M., Komatsu T., Sugano S., Rombari R., Radamata M., Rayamura Y., Ohara O., Isogai T., Satoh T., Satoh T., Satoh T., Shita Y., Yamashita R., Pulakami R., Yada T., Nakamura Y., Ohara O., Isogai T., Satoh S., Satoh J., Sa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Name=drpr; ORFNames=CG2086;

Drosophila melanogaster (Fruit fly).

Bukaryota; Matazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Endopteraygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match
Local Similarity 57.9%; Pred. No. 36;
les 11; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nat. Genet. 36:40-45(2004).
EMBL, AK022609; BAB14128.1; -.
SEQUENCE 307 AA, 32780 MW; 4CC18ACD39BD3AC3 CRC64;
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Matches
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Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., A Glodek A., Gong F., Garg N.S., Gelbart W.M., Glasser K., A Glodek A., Gong F., Gorrell J.H., Gu Z., Glan P., Harris M., Aarush F., Garrell J.H., Gu Z., Glan P., Harris M., Aarush F., Karben G.H., Wei M.H., Ibegwam C., A Jaali M., Kalush F., Karpen G.H., Kez, Kannison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Martei B., McIntosh T.C., Morris J., Moshrefi A., Markei B., McIntosh T.C., Morris J., Moshrefi A., Markei B., McIntosh T.C., Morris J., Moshrefi A., Markun G.S., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Malson D.K., Nelson K., Naxon K., Naskar D.B., Palazzolo M., Pittman G.S., Naxon K., Pollard J., Puri V., Reese M.G., Raniazolo M., Stungki M., Schoeler F., Shen H., Shen B.C., Siden-Kiamos I., Simpson M., Skrupski M., Smith T., Spier B., Spradling A.C., Stapleton M., Strong R., Sun E., Spier B., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.Y., Wassaman D.A., Weinscock G.M., Weissenbach J., Weinscock G.M., Weissenbach J., Zhong W., Zhong W., Zhong G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon S., Zhon X., Zhon S., Zhon X., Zhon S., The genome sequence of Drosophila melanogaster.",

Science 287:2185-2195(2000).
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MEDLINE=22426065; PubMed=12537568;

MEDLINE=22426065; PubMed=12537568;

Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Patk S., Peiffer B.D., Richards S., Sodergren B.J., Neinstas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence.";

Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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MEDLINE=22426070; PubMed=12537573;
Raminker J.S., Bergaman C.M., Kronmiller B., Carlson J., Svirskas R.,
Raminker J.S., Bergaman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel B., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-22446069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huany Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003472; AAF47553.2; -
HSSP; Q12780; 1HAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
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GO; GO:0008345; P:larval locomotory behavior; IMP.
InterPro; IPR000742; EGF 2.
InterPro; IPR006209; EGF 1ike.
InterPro; IPR003006; IG_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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Jenome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
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Gaps
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anopheles Genome Sequencing Consortium;
Submitted (APR-2003) to the EVBL/GenBank/DDBJ databases.

-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is nerero: IPR0010192; Asx. hydroxyl_S.

R InterPro: IPR00152; Asx. hydroxyl_S.

InterPro: IPR001791; Edmlinn_G.

R InterPro: IPR001791; Laminin_G.

R InterPro: IPR001791; Daminin_G.

R InterPro: IPR001791; Sushi_SCR_CCP.

R InterPro: IPR001485; Sushi_SCR_CCP.

R Pfam; PF00008; EGF_S.

R Pfam; PF00494; HYR; 2.
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                                                                                                                                                                                                                                                                                                                            2; Length 881;
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                                                                                                                                                                                                                                                                      96380 MW; 52196D164F52F5C1 CRC64;
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01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1823 AA.
                                                                                                                                                                                                                                                                                                                         47.3%; Score 53; DB
llarity 64.3%; Pred. No. 91;
Conservative 3; Mismatches
                    Ffam; PF00008; EGF; 1.

PFAm; PF00008; Laminin. EGF; 6.

PRINES; PR00011; EGFLAMINN.

SMART; SM00180; EGFLAM; 3.

PROSITE; PS00102; EGF_1; 11.

PROSITE; PS01086; EGF_2; 13.

PROSITE; PS0026; EGF_3; 7.

Laminin EGF-1ike domain.

SEQUENCE 881 AA; 96380 MW; 52196D16
InterPro; IPR002049; Laminin_EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Fragment).
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Pfam; PF00092; VWA; 1.
PRINTS; PR00895; PENTAXIN.
PRINTS; PR00453; VWFADOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    409 RCVCKQDWGVCRCL 422
                                                                                                                                                                                                                                                                                                                                                                                                                                       4 RCLCRR--GVCRCL 15
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                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity (
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Functional annotation of a full-length mouse cDNA collection.";
             Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                 MEDLINE=22789168; PubMed=12907728; MacLeod A., Bringaud F., El-Sayed N.M.A., Ghedin E., Song J., MacLeod A., Bringaud F., El-Sayed N.M.A., Ghedin E., Song J., MacLeod A., Bringaud F., Tweedie A., Biteau N., Khalak H.G., Lin X., Mason T., Hannick L., Caler E., Blandin G., Bartholomeu D., Simpson A.J., Kaul S., Zhao H., Pai G., Van Aken S., Utterback T., Haas B., Koo H.L., Umayam L., Sub B., A Gerrard C., Leech V., Qi R., Zhou S., Schwartz D., Feldblyum T., Salzberg S., Tait A., Turner M.R., Uilu E., White O., Melville S., Adams M.D., Fraser C.M., Donelson J.E.; White O., Melville S., Invieic Acids Res. 31:4886-4863(2003).

Mydochetical protein.
                                                                                                                                                                                                                    Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Trypanosoma
NCBI_TaxID=5691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR.2003 (TrEMBLrel. 23, Created)
01-MAR.2004 (TrEMBLrel. 23, Last sequence update)
01-MAR.2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 3 days neonate thymus CDNA, RIKEN full-length enriched library, clone:A630032M05 product:hypothetical protein, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                           46.9%; Score 52.5; DB 2; Length 101; 56.2%; Pred. No. 16; 2; Mismatches 2; Indels 3
      Length 1823;
                          6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               l protein.
101 AA; 10880 MW; E63D8E62A9CA6748 CRC64;
                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
   47.3%; Score 53; DB 2; 56.2%; Pred. No. 1.7e+02; ive 1; Mismatches 6
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STRAIN=CS7BL/6J; TISSUE=Thymus;
MEDLINE=99279223; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 AA.
                                                                                                                                101 AA
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MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM CONSOTTIUM;
                                                                                                                                PRT;
                                                                                                                                                  ".-vcT-2003 (TrEMBLrel. 25, C)
01-0CT-2003 (TrEMBLrel. 25, La
Hypochetical protein.
ORFNames=Tb927.2.4940;
Trypanosoma bruce.
                                                                      262 VCSCLTTSGHYRCICK 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16
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                                                   2 VCRCLCRRGVCRCLCR 17
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Best Local Similarity 56.2.
Best Local 9; Conservative
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      Query Match
Best Local Similarity 56.2
Matches 9; Conservative
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                                                                                                                                PRELIMINARY;
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Q8C9N2
                                                                                                           RESULT 32
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

CARACHI, O., Aizawa K., Akimurat., Hara A., Hashizume W.,
Adachi J., Ruruno M., Haragaki T., Hara A., Hashizume W.,
Rukuda S., Furuno M., Hiramoto K., Hiraoka T., Hirozane T.,
A. Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
A. Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A. Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Konda M., Koya S.,
A. Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
A. Nomura K., Numuzaki R., Ohno M., Ohsacume N., Okazaki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Saibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,
A. Tagawa A., Takhashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu W., Hayashizaki Y.;
Submitted (JUL-2001) to the BML/GenBank/DDBJ databases.

EMBL; AKO41730, AK
                                                                                                                                                                                                                                                                                                                                                                                                                               SECUENCE FROM N.A.
STRAIR-CAPEL/GJ; TISSUE=Thymus;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
"Normalization and subtraction of Cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000)
                                                                                                   The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team,
the RIKEN Genome Exploration Research Group Phase I & II Team,
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length CDNAs.",
Nature 420:563-573(2002).
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STRAIN=C57BL/6J; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagooka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishir K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M., Oneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., "RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002453; Beta_tubulin.
PROSTIE; PS00228; TUBULIN_B_AUTOREG; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 118 AA; 13452 MW; CA98EICGB01CD77F CRC64;
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
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Best Local Similarity 50...

...a 9; Conservative
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product:hypothetical protein, full insert sequence.
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Best Local Similarity
Matches 9; Conserv
  1;
                                             Sharov A.A., Piao Y., Matoba R., Dudekula D.B., Qian Y., VanBuren V., Sharov A.A., Piao Y., Stagg C.A., Bassey U.C., Wang Y., Carter M.G., Hamatani T., Aiba K., Akutsu H., Sharova L., Tanaka T.S., Kimber W.L., Yoshikawa T., Jaradat S.A., Pantano S., Nagaraja R., Boheler K.R., Yoshikawa T., Jaradat S.A., Pantano S., Nagaraja R., Boheler K.R., Taub D., Hodes R.J., Longo D.L., Schlessinger D., Keller J., Klotz E., Kelsoe G., Umezawa A., Vescovi A.L., Rossant J., Kunath T., Hogan B.L., Curci A., D'Urso M., Kelso J., Hide W., Ko M.S., "Transcriptome analysis of mouse stem cells and early embryos."; EMBL, AYS12913, AAR87784.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sharov A.A., Fiao Y., Matoba R., Dudekula D.B., Qian Y., VanBuren V., Falco G., Martin P.R., Stagg C.A., Basey U.C., Wang Y., Catter M.G., Hamatani T., Aiba K., Akutsu H., Sharova L., Tanaka T.S., Kimber W.L., Yoshikawa T., Jaradat S.A., Pantano S., Nagaraja R., Boheler K.R., Taub D., Hodes R.J., Longo D.L., Schlessinger D., Keller J., Klotz E., Hogan B.L., Curci A., Vescovi A.L., Rossant J., Kunath T., Hogan B.L., Curci A., D'Urso M., Kelso J., Hide W., Ko M.S., "Transcriptome analysis of mouse stem cells and early embryos."; PLOS Biol. 1:410-419(2003)
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last amnotation update)
Mus musculus 11 days pregnant adult female ovary and uterus cDNA,
RIKEN full-length enriched library, clone:5031438A03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 133 AA; 14583 MW; 5929328D1A4B4BF7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                  133 AA
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Pred. No. 20;
                                                                                                                                                                                                                                                 1; Mismatches
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                                                                                                                                                                                                                           46.9%;
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Conservative
                                                                                                                                                                                                                                                                         2 VCRCLCRRGVCRCLC 16
                                                                                                                                                                                                                                                                                                 57 VCMCLC---VCLCVC 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VCRCLCRRGVCRCLC 16
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                                                                                                                                                                                                                        Query Match
Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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SEOUENCE 133 AA; 1
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Best Local Similarity
Matches 9; Conserv
                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                              AAR87784;
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RC STRAIN-CSTBL/61; TISSUB=Ovary and uterus;
Adachi J. Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J. Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda K., Furuno M., Hangaki T., Haracka T., Hirozane T., Hayatsu N., Hiracka T., Hirozane T., Adashida K., Ishii Y., Itoh M., Kagawa I., Kaukawa T., Kanch H., Kawai J., Kojima Y., Kono M., Kagawa T., Kayawa T., Miyazaki A., Murata M., Nakamura M., Airihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Oksato H., Sakai D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T., Arawahashi F., Takaku-Akahira S., Takakai Y., Tanaka T., Amaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Shinagawa A., Shiraki K.) Shinagawa A., Shiraki T., Sogabe Y., Tanaka T., Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

R. EMBL, AKOTYST; BAG36119.1;
R. PMBL, AKOTYST; BAG36119.1;
R. PMBL, AKOTYST; BAG36119.1;
R. PMBL AKOTYST; BA
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STRANIE-STREICH, G.J. TISSUE=Ovary and uterus;
The FANTOM CONSORtium.
The RIKEN Genome Exploration Research Group Phase I & II Team;
Thanalysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Mature 420:563-573 (2002).
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STRAIN-G7SPBL/64) TISSUE-Ovary and uterus;
STRAIN-G7SPBL/64) TISSUE-Ovary and uterus;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama V., Nishi K., Kitaunai T., Tashihro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazawa M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watsunia K.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RIKEN integrated sequence analysis (RISA) system-384-format
Genome Res. 10:1757-1771(2000).
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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146 AA; 16179 MW; 711E0C93EC80DBBB CRC64;
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STRAIN-C57BL/6J; TISSUB=Ovary and uterus;
MEDLINE=99279253; Pubmed=10349636;
Carnino: P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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TYRAIN=CSPEL/GJ, TISSUE=Ovary and uterus;
MEDLINE=11085660; PubMed=11217851;
RIKEN FANTOM CONSORTIUM;
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Gaps

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Indels

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419 GVCVCVC---VCVCVC 431
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[2]
SEQUENCE FROM N.A.
TISSUE=Whole;
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SEQUENCE
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QBIRLO;
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Matches
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QBIRLO
ID QBIRLO
AC QBIRLO
     MEDINE-2238257; PubMed=12477932;

MEDINE-2238257; PubMed=12477932;

MEDINE-2238257; PubMed=12477932;

MEDINE-2238257; PubMed=12477932;

MEDINE-2238257; PubMed=12477932;

MAISCALL S.P., Collins R.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B.E., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Gasavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., McZwan P.J., McKernan K.J., Malek J.A., Glubs R.A.,

Brownstein M.J., Halton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Minish M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human

"Generation and initial analysis of more than 15,000 full-length human

"The proc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUB-Human small intestine;
TISSUB-Human small intestine;
Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
Watanabe K., Chayashi M., Nishi T., Shibahara T., Tanaka T.,
Nakamura Y., Isogai T., Sugano S.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO26249; BAB15412.1;
SEQUENCE 160 AA; 16738 MM; FBBB34293CBEZTET CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygli; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                               01-MAR-2001 (TrEWBLrel. 16, Created)
01-MAR-2001 (TrEWBLrel. 16, Last sequence update)
01-OCT-2002 (TrEWBLrel. 22, Last annotation update)
Hypothetical protein FLJ22596.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 56.2%; Pred. No. 24;
Matches 9; Conservative 2; Mismatches 2; Indels ...
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein (Fragment)
                                                                                                                                                                       PRT; 160 AA.
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                          96 VCMCVC---VCVCVCMR 109
2 VCRCLCRRGVCRCLCRR 18
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                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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Q9H654;
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Q6GQP2;
                                                                                                              RESULT 37
29465
AC 09465
AC 09465
DT 01-MA
DT 01-MA
DT 01-OC
DE HYPOT
OC BUKAR
OC MAMMA
OC MAMMA
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OC MAMMA
RA WATAN
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RA WATAN
RA WATAN
RA NAKAN
RA NA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=CO6Al.6;
Caenorhabditis elegans.
Bukaryota; Metasoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                           3,
                                                                                                                                                                                         DB 2; Length 462;
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Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
R BRBL; Z49886; CAA90055.1; -
R PIR; T18975; T18975.
R WormPep; CO6A1.6; CE20484.
R WormPep; CO6A1.6; CE20484.
R InterPro; IPR001450; 4Fe45 ferredoxin.
R InterPro; IPR001450; AFe45 ferredoxin.
R InterPro; IPR001450; AFe45 ferredoxin.
R InterPro; IPR00195; EndoIII FCL.
R InterPro; IPR00195; EndoIII FCL.
R PROSITE; PS001095; BGF 1; UNKNOWN 1.
R PROSITE; PS00102; BGF 1; UNKNOWN 1.
R PROSITE; PS00108; VWFC_1; 1.
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Science 282:2012-2018(1998),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 52.9%; Pred. No. 26;
Matches 9; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                           2; Indels
Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC072700; AAH72700.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           al protein.
152 AA; 15646 MW; 6E254F0BE476D354 CRC64;
                                                                                                                                      462 AA; 52504 MW; 9BF8B5754E98355A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1999 (TrEMBLrel. 12, Created)
(1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein C06A1.6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 152 AA.
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Local Similarity 56.2%; Pred. No. 60;
les 9; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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RADINEZ-DISCOSE PROM N.A.

RADINEZ-DISCOSE PROM N.A.

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

RA Gutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Bardon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C.R., Gabor Gl.,

RA Abril J.F., Agbayani A., Barendan B.P., Bhandari D., Bolshakov S.,

Barkova D., Botchan M.R., Bouck J., Bhandari D., Bolshakov S.,

Burtis R.C., Busam D.A., Burtler H., Bhandari D., Bolshakov S.,

Burtis R.C., Busam D.A., Partler H., Cadieu E., Center A., Chandra I.,

RA Burtis R.C., Busam D.A., Burtler H., Cadieu E., Center A., Chandra I.,

RA Burtis R.C., Busam D.A., Burtler H., Davies P.,

RA Bodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C.,

Burtis R.C., Gabrielian A.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RA Burtis N.L., Raviellista C.C., Ferraz C., Ferriar S., Fleischman W.,

RA Gloder C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser X.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Harris M.,

RA Glode A., Gong F., Gorrell J.H., Gu Z., Genbart W.M., Ketchum K.A.,

RA Harris N.L., Matther B.W., Karpen G.H., Kez Z., Kennigon J.A., Ketchum K.A.,

RA Harris N.L., Matther B.W., Karpen G.H., Kez Z., Kennigon J.A., Ketchum K.A.,

RA Harris N.L., Levitsky A.A., Li J.J., Liang Y., Lin X.,

RA Melson D.R., Noly M., Murphy B., Murphy L., Murshy D.M., Noshrei A.,

Reiner K., Remindton K.A., Ban S., Pollard J., Puri V., Reese M.G.,

Raber E., Siden-Kamos I. S., Sungeon M., Strong R., Sunt E.,

Raber E., Siden-Kamos I. S., Sungeon M., Strong R.,

Raber E., Siden-Kamos I. S., Sungeon M., Strong R.,

Raber S., Ravis S.M., Woodager, Worley R.M., Weissenbach J.,

Raber S., Ravis S.M., Woodager, Worley S., Weiter S., Wall H. W.,

Raber S., Ravis S., Ravis R.
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=22426065; PubMed=12537568;

Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,

Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,

Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

Pacleb J.M., Park S., Men K., Stapleton M., Sutton G.G., Venter C.,

Weinstock G., Scherer S.E., Myers B.W., Gibbs R.A., Rubin G.M.;

"Finishing a whole-genome shotgun: release 3 of the Drosophila
                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
CG32681-PA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The genome sequence of Dross Science 287:2185-2195(2000).
                                                                                                                                                                                                                             ORFNames=CG32681;
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SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise B., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.,
Ashburner M., Celniker S.E.,
"The transposable elements of the Drosophila melanogaster euchromatin:

Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).

genomics perspective."

melanogaster euchromatic genome sequence."; Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

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Gaps
SEQUENCE FROM N.A.

Mibrine=22426669; PubMed=12537572;

Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B.,

Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,

Bettencourt B.R., Celniker S.B., de Grey A.D., Drysdale R.A.,

Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                          "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
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                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases. EMBL, AE003450; AAN09260.1; -1 Flybase, Egno0525681; CG32681; SEQUENCE 1506 AA; 169457 MW; 13193417CFAA9772 CRC64;
                                                                                                                                                                                                                                                                                          to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                systematic review.";
Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
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Search completed: October 26, 2004, 15:39:22 Job time : 130.5 secs

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us-10-009-317a-33.rag

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di ·	LOSUM62 apop 10.0 , Gapext 0. 002273 seqs, 35872929 its satisfying chosen ngth: 0	ocessing: Minimum Match 0% Maximum Match 100 Listing first 45	Database: A_Geneseq_23Sep04:*  1: geneseqp1980s:* 2: geneseqp1990s:* 3: geneseqp2000s:* 4: geneseqp2001s:* 5: geneseqp2001s:* 6: geneseqp2003s:* 7: geneseqp2003bs:* 8: geneseqp2003bs:*	sults pre the sco	SUMMARIES  \$ Query No. Score Match Length DB ID  Description	112 100.0 18 4 AAB35047 AAD3504 112 100.0 18 5 ABP53296 Ad0352 112 100.0 18 8 AD035231 Ad0352 112 100.0 18 8 AD035242 Ad0352 107 95.5 18 8 AD035241 Ad0352 107 95.5 18 8 ABP53298 Ad0352 108 91.1 18 5 ABP53298 Ad0353 99 88.4 18 5 ABP53297 Adp532	10 99 88.4 18 6 AAB23866 AAB23866 AAB23866 Madaca mu 11 99 88.4 18 7 ADD55357 AAG35520 Cyclic de 12 99 88.4 18 8 ADD55357 AAG470012 AG435557 Antimicro AG470012 AG435557 Antimicro AG470012 AG435557 Antimicro AG470012 AG435557 Antimicro AG470012 AG

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Anti-viral; viral infection; theta-defensin; lipid environment; amphipathic alpha-helical structure; virucide; anti-HIV; immunisation; viral growth inhibitor; viral proliferation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roller R, Mccray PB,
                                                                                                                                                     Anti-viral theta defensin peptide RTD-3 SEQ ID NO:29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stinski M,
ABP53296 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9-JAN-2002; 2002WO-US002435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-2001; 2001US-0265270P.
01-AUG-2001; 2001US-0309368P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IOWA ) UNIV IOWA RES FOUND.
                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maury W, Stapleton J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-674815/72.
                                                                                                                                                                                                                                                                                                              Macaca mulatta.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                         WO200260468-A2.
                                                                                                   13-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                             38-AUG-2002,
                                                 ABP53296;
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New method of using a first anti-viral peptide comprising a Theta-defensin peptide in an amphipathic Alpha-helical structure in a lipid environment for reducing the infectivity of a virus.

Disclosure; Page 10; 65pp; English.

peptide (I) comprising a theta-defensin peptide in an amphipathic alphanolical structure in a lipid environment for reducing the infectivity of a virus. (I) can have virucide and anti-HIV activities, and can be used to reduce virus growth, infectivity burden, shed, and development of anti-LIV activities, and so can be used for; (a) protecting or treating subject from a viral infection, preventing recurrent viral infection in a subject harbouring a latent virus, controlling virus infection in a subject harbouring a latent virus, controlling virus special protects subject (vs), reducing virus shed from a vs. reducing percentage of Vs in a Vs. reducing virus shed from a vs. reducing percentage of Vs in a population regardless of viral infection status, or inducing latency in a Vs. (b) reducing the infectivity of a virus, and (c) rendering virus shed from a vs. reducing the number contaminated tissue or fluid sample safe for use, or reducing the number of virus infections virus particles in a population of viruses. (MI) is useful for reducing the infectivity of a virus in sheep, cattle, horses, swine, cats, fewl and humans e.g. an enveloped virus infection humans e.g. an enveloped virus infection who is ministered to a patient who is immunosuppressed to a constant peptide is administered to a patient who is immunosuppressed to a subject who is anti-viral peptide is most preferably administered to a subject who is contaminated represents a rhesus monkely thet a virus. The present sequence represents a rhesus monkely thet a virus in peptide, which is given in the exemplification of the present invention The present invention describes a method (M1) of using a first anti-viral

Query Match

ö Gaps ö 100.0%; Score 112; DB 5; Length 18; 100.0%; Pred. No. 9.2e-06; ... ive 0; Mismatches 0; Indels Conservative Best Local Similarity Matches 18; Conserval

GVCRCLCRRGVCRCLCRR 18

AD03523

ADO35231 standard; peptide; 18

(first entry) 15-JUL-2004

Rhesus theta defensin peptide, RTD-3.

Monkey, Rhesus theta defensin, RTD-3, antimicrobial peptide, cyclic, antimicrobial, antinflammatory, antibacterial, virucide, fungicide; food, contact lens solution, eye wash solution; inflammatory response, microbicidal inhibition, microbistatic growth inhibition, disinfectant, food preservative, bacterial infection, viral infection, thection, fundal infection, 

Macaca mulatta.

 .18
 .nte= "The peptide is cyclised by a covalent link between these two residues" Location/Qualifiers Key Modified-site

Disulfide-bond Disulfide-bond Disulfide-bond

US2004014669-A1

B

22-JAN-2004.

30-APR-2003; 2003US-00427715.

30-APR-2002; 2002US-0377071P

(REGC ) UNIV CALIFORNIA.

Selsted ME, Tran DQ;

WPI; 2004-167945/16.

Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate object.

Example 1; SEQ ID NO 3; 46pp; English.

The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as AD035239-AD03527. The theta defeatiled in the claims or appearing as AD035239-AD035257. The theta defeatiled in the claims or appearing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of a microorganism in an environment such as food or growth or survival of a microorganism in an environment such as food or solution, an inanimate object comprising surface, or a mammal. The solution, an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present high antimicrobial activity and low haemolytic activity. The present sequence represents the rhesus monkey wild-type theta defensin RTD-3

Sequence 18 AA;

100.0%; Score 112; DB 8; Length 18; 100.0%; Pred. No. 9.2e-06; Query Match Best Local Similarity m

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Gaps

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Rhesus theta defensin analogue peptide aRTD-3-NH. Claim 1; SEQ ID NO 16; 46pp; English. ADO35242 standard; peptide; 18 AA. 1 GVCRCLCRRGVCRCLCRR 18 GVCRCLCRRGVCRCLCRR 18 30-APR-2003; 2003US-00427715. 30-APR-2002; 2002US-0377071P. (first entry) 18; Conservative (REGC ) UNIV CALIFORNIA 3. .16 5. .14 7. .12 Tran DQ; WPI; 2004-167945/16. Disulfide-bond Disulfide-bond Disulfide-bond Modified-site US2004014669-A1 Seguence 18 AA Macaca mulatta Selsted ME, 15-JUL-2004 Synthetic object. Matches AD035242 ਨੇ

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the invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO3529-ADO3527. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of a microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or growth or survival of a microorganism in an environment such as food or old the product, as solution (e.g., contact lens solution, or eye wash solution), an innimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbistatic inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as the repetides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monkey; Rhesus theta defensin, RTD; antimicrobial peptide; antimicrobial; antiinflammatory; antibacterial; virucide; fungicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial infraction; viral infection; disinfectant; fungal infection; haemolytic activity.
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               100.0%; Score 112; DB 8; Length 18; 100.0%; Pred. No. 9.2e-06; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                         ADO35241 standard; peptide; 18
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                                            Best Local Similarity
Matches 18; Conserv
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Disulfide-bond
Disulfide-bond
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                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO35257. The theta defensin nalogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of survival of microorganism as well as microbistatic inhibition of survival of microorganism as well as therapeutic agents, disinfectants, food preservatives, or medicaments.
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                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel theta defensin analog useful for reducing or inhibiting growth survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
                                                                                                      .
sequence represents a Rhesus theta defensin analogue peptide.
                                                                  Length 18;
                                                                                                                                                                                                                                                                                                                                                                    Rhesus theta defensin analogue peptide 3:1 aRTD-1-NH.
                                                                100.0%; Score 112; DB 8;
100.0%; Pred. No. 9.2e-06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 17; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                               Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Amidated"
                                                                                                                                                                                                                                                              ADO35243 standard; peptide; 18
                                                                                                                                       18
                                                                                                                                                                        18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-APR-2002; 2002US-0377071P.
                                                                                                                                       1 GVCRCLCRRGVCRCLCRR
                                                                                                                                                                      1 GVCRCLCRRGVCRCLCRR
                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tran DQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-167945/16.
                                                                                   Local Similarity
Les 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disulfide-bond
Disulfide-bond
Disulfide-bond
                                 Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2004014669-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macaca mulatta.
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                                                                                                                                                                                                                                                                                                                                15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Selsted ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-JAN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                               AD035243;
                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      object.
                                                                                                      Matches
                                                                                                                                                                                                                                               AD035243
                                                                                                                                                                                                                            RESULT
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The present invention describes a method (M1) of using a first anti-viral peptide (I) comprising a theta-defensin peptide in an amphipathic alphanelus althoughes in a lipid environment for reducing the infectivity of a virus. (I) can have virucide and anti-HIV activities, and can be used to reduce virus growth, infectivity burden, shed, and development of anti-viral resistance. (I) can be used for inhibiting the growth and proliferation of a virus and so can be used for; (a) protecting or reating subject from a viral infection, preventing recurrent viral infection in a subject harbouring a latent virus, controlling virus pread within a virally-infected subject (VS) reducing virus alted from a VS. reducing percentage of VS in a vS, reducing virus shed from a VS. reducing percentage of VS in a vS; (b) reducing virus shed from a virus infection status, or inducing latency in a VS; (b) reducing the infectivity of a virus; and (c) rendering virus-contaminated tissue or finid sample safe for use, or reducing the number of infectious virus particles in a population of viruses. (M1) is useful for reducing the infectivity of a virus in sheep, cattle, horses, swine, catts, fowl and humans e.g. an enveloped virus infecting humans such as human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-viral, viral infection, theta-defensin, lipid environment, amphipathic alpha-helical structure, virucide, anti-HIV, immunisation, viral growth inhibitor, viral proliferation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New method of using a first anti-viral peptide comprising a Theta-defensin peptide in an amphipathic Alpha-helical structure in a lipid environment for reducing the infectivity of a virus.
The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theca defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents a Rhesus theta defensin analogue peptide.
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-viral chimeric theta defensin peptide H/RTD-3 SEQ ID NO:31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tack
                                                                                                                                                                                 0
                                                                                                                                         Score 107; DB 8; Length 18;
Pred. No. 3.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mccray PB,
                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roller R,
                                                                                                                                                     100.08; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stinski M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 10; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                           ABP53298 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                       GVCRCLCRRGVCRCLCR 18
                                                                                                                                                                                                                    1 GVCRCLCRRGVCRCLCR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JAN-2002; 2002WO-US002435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001US-0265270P.
                                                                                                                                         95.5%;
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                                                                                                                        Query Match
Best Local Similarity 100.0
....hes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-674815/72.
                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mulatta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200260468-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                      13-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                   Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Macaca mul
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                 ABP53298;
                                                                                                                                                                                                                                                                                                                    RESULT 7
                                                                                                                                                                                                                                                                                                                                         ABP53298
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GFCRCLCRRGVCRCICTR 18

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administered to a patient who is immunosuppressed or to a subject who is not infected with the virus, where the first anti-viral peptide is administered prior to or subsequent to the virus contacting the subject. The anti-viral peptide is most preferably administered to a subject who is chronically, latently or acutely infected with the virus. The present sequence represents a chimeric human/rhesus monkey thera defensin anti-viral peptide, which is given in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides theta defensin peptides and analogues which have antimicrobial activity. They can be used in the treatment bacterial, viral, fungal, protozoan and helminthic infections, in disinfectants and as food preservatives
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cyclic; bacterium; fungus; protozoan; food preservative; analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel theta defensin peptide with antimicrobial activity against
bacteria, yeast, fungi, protozoa and viruses.
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    .18
/note= "peptide bond cyclises the molecule"

                                                                                                                                                                              Query Match 91.1%; Score 102; DB 5; Length 18; Best Local Similarity 83.3%; Pred. No. 0.00011; Matches 15; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 88.4%; Score 99; DB 4; Length 18; Local Similarity 83.3%; Pred. No. 0.00023; es 15; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouellette AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 4; 110pp; English.
                                                                                                                                                                                                                                                             1 GICRCLCRRGVCRCICGR 18
                                                                                                                                                                                                                                           1 GVCRCLCRRGVCRCLCRR 18
                                                                                                                                                                                                                                                                                                                                                    AAB35030 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Theta defensin; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               virus; helminth; disinfectant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yuan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAY-2000; 2000WO-US012842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-00309487
                                                                                                                                                                                                                                                                                                                                                                                                                                                Theta defensin SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-031853/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18 AA;
                                                                                                                                                  Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200068265-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .0-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                   27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-links
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                                                                                                                                                                                                                                                                                                                                                                                     AAB35030;
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The present invention describes a method (M1) of using a first anti-viral peptide (I) comprising a theta-defensin peptide in an amphipathic alphabelic peptide (I) comprising a theta-defensin peptide in an amphipathic alphabelic structure in a lipid environment for reducing the infectivity of a virus. (I) can have virucide and anti-HIV activities, and can be used for inhibiting the growth and conce viral seasons. (I) can be used for inhibiting the growth and proliferation of a virus and so can be used for; (a) protecting or treating subject from a viral infection, preventing recurrent viral infection in a subject harbouring a latent virus, controlling virus in spread within a virally infected subject (VS). Reducing virus shed form a Viracian percentage of VS in a contaminated tissue or fluid sample safe for use, or reducing the number of infectious virus particles in a population of viruses. (M1) is useful for infectious virus particles in a population of viruses. (M1) is useful for for reducing the infectivity of a virus; and (c) rendering virus supported for a patient who is number of cats, fowl and humans e.g. an enveloped virus infecting humans such as human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is administered prior to or subsequent to the virus contacting the subject. The anti-viral peptide is most preferably administered to a patient where the first anti-viral peptide is most preferably administered to a patient where the first anti-viral peptide is contacting the virus. The present sequence represents a thesus monkey there defensin anti-viral peptide, which is given in the exemplification of the present invention
                                                                                                                                                                                                   Anti-viral; viral infection; theta-defensin; lipid environment; amphipathic alpha-helical structure; virucide; anti-HIV; immunisation; viral growth inhibitor; viral proliferation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New method of using a first anti-viral peptide comprising a Theta-defensin peptide in an amphipathic Alpha-helical structure in a lipid environment for reducing the infectivity of a virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tack B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.4%; Score 99; DB 5; Length 18; 83.3%; Pred. No. 0.00023; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mccray PB,
                                                                                                                                                                 Anti-viral theta defensin peptide RTD-1 SEQ ID NO:30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roller R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stapleton J, Stinski M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 10; 65pp; English.
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01-AUG-2001; 2001US-0309368P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IOWA ) UNIV IOWA RES FOUND.
                                                                                                                       (first entry)
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Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 AA;
                                                                                                                                                                                                                                                                                               mulatta.
                                                                                                                                                                                                                                                                                                                                                         WO200260468-A2.
                                                                                                                       13-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                    08-AUG-2002
                                                                                                                                                                                                                                                                                             Macaca mul
Synthetic.
                                                                                ABP53297;
                                      ABP53297
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RESULT 9
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Gaps

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Gaps

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1 GVCRCLCRRGVCRCLCRR 18

Query Match

Best Loca Matches

bacterial infection; human pathogen; holin; defensin; peptide nucleic acid; PNA; penicillin; tetracycline; ampicillin; kanamycin; antibiotic; antibacterial; antibiotic-resistance gene; cyclic.

Unidentified

Cyclic defensin fragment.

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The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroival infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin-mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is rheav monkey theta defensin, RTD1 peptide. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                   Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV; human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; rhesus monkey; theta defensin 1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually transmitted diseases, vaginosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 99; DB 6; Length 18;
Pred. No. 0.00023;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Fig 3C; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cole AM,
                                                                                                  AAE33866 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADD95202 standard; peptide; 18
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83.3%;
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GVCRCLCRRGVCRCLCRR
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                                                                                                                                                                                       Macaca mulatta RTD1 peptide
                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waring AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-103387/09.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18 AA;
                                                                                                                                                                                                                                                                                              Macaca mulatta
                                                                                                                                                                                                                                                                                                                            WO200285401-A1
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                                                                                                                                                              16-APR-2003
                                                                                                                                                                                                                                                                                                                                                          31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lehrer RI,
                                                                                                                                  AAE33866;
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ADD95202
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                                                                         RESULT 10
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This invention describes a novel conjugate for treating prokaryotic infections which comprises a transport mediator for passage through the prokaryote call membrane and a compound, directed against a prokaryote prokaryote and intended for introduction into it. The prokaryote is a bacterium, especially one pathogenic in humans. The transport mediator is preferably a human peptide or protein, especially a phage-holin protein, its active fragment or variant or a defension. The introduced compound is a peptide nucleic acid (PNA) that inhibits a gene, especially one implicated in resistance to penicillin, terracycline, ampicillin or kanamych. The conjugate has the structure transport mediator-spacer-PNA where the spacer is linked to the transport mediator through a cileavable disulfide bridge. The conjugates are administered together with an antibiotic, by parenteral, transdermal or subcutaneous routes. The products of the invention have antibacterial activity and are used, especially in combination with antibiotics, for treating prokaryotic, specifically bacterial, infections, especially where the pathogen is resistant to at least one antibiotics and the antibiotics can entibiotic resistance gene where the PNA is directed against the antibiotic resistance gene: Where the PNA is directed against antibiotic resistance gene: Where the PNA is directed against entibiotic resistance gene: Where he PNA is directed against sequence represents a cyclic defensin fragment described in the very sequence represents a cyclic defensin fragment described in the current or the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New conjugate of transport mediator and active agent, useful for treating prokaryotic infections, especially by neutralizing antibiotic resistance

    .18
/note= "Residue 1 and residue 18 bond to form a cyclic

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waldeck W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Debus J, Pipkorn R,
                                                                                                                                                                                                                                                                                                                                                                                                                                       (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 10; 34pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18
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                                                                                                                                                                                                                                                                                                                                                               17-JAN-2003; 2003WO-DE000124
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Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                               moiety"
3. .16
5. .14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Braun K, Braun I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-689464/65
                                                                                                                                                                                                                Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                          WO2003059392-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18 AA;
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RESULT 12

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ADD35357 ID ADD3 XX

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for preparing a composition for treatment and/or prevention of bacterseamia for binding bacterial products such as lipopolysaccharide bacteranial for binding bacterial products such as lipopolysaccharide of septic shock. RTD-1, isolated from immune cells of rhesus monkeys, has antibacterial, fungicide, virucide, immunomodulator and anticoagulant activity. RTD-1 inhibits microbial cell-wall biosynthesis and also binds to LPS and LTA. RTD-1 is useful for treatment and prevention of severe by viruses. RTD-1 combines four advantageous properties: a direct antimicrobial action, neutralisation of bacterial products (by binding), immunomodulation (reducing release of proinflammatory cytokines but increasing release of regulatory factors) and anticoagulant action, so provides a better and simpler treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes the novel use of rhesus theta defensin-1 (RTD-1)
                                                                                                                                                                                                                                                                                                                                                                                                            Use of rhesus theta defensin-1 for treating or preventing bacteremia and septic shock, also for binding bacterial products and as immunomodulator and anticoagulant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Monkey, Rhesus theta defensin, RTD-1; antimicrobial peptide; cyclic; antimicrobial; antiinflammatory; antibacterial; virucide; fungicide; food; contact less solution; eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; fungal infection;

    .18
hotte= "The peptide is cyclised by a covalent link
between these two residues"

microbial cell-wall biosynthesis; immunomodulation; anticoagulant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 99; DB 8; Length 18;
Pred. No. 0.00023;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                         Brunner N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhesus theta defensin peptide, RTD-1.
                                                                                                                                                                                                                                                                                                                         Labischinski H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; SEQ ID NO 1; 28pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADO35229 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18
                                                                                                                                                                                                                                  13-JUN-2002; 2002DE-01026216
                                                                                                                                                                                   30-MAY-2003; 2003WO-EP005694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 83.3%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GVCRCLCRRGVCRCLCRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                             (FARB ) BAYER HEALTHCARE
                                                                                                                                                                                                                                                                                                                         Newton B,
                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-071500/07
                                                                                            WO2003105883-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AD035229;
                                                                                                                                                                                                                                                                                                                         Ladel C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel ophthalmic solution comprising a prostaglandin of the F-series and an antimicrobial peptide. A solution of the invention has hypotensive and ophthalmological activity. The solution is useful for the treatment of increased intraccular pressure, such as prostaglandin and the antimicrobial peptide work synergistically, to provide beneficial reduction in the incidence of irritant and toxic side effects such as hyperaemia, irritation and inflammation of conjunctiva, coular call dysplasia, irritation and inflammation of conjunctiva, hyperplementation, associated with the prior art prostaglandin compositions. The present sequence represents an antimicrobial peptide of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rhesus theta defensin-1; RTD-1; bacteraemia; lipopolysaccharide; LPS;
lipteichonic acid; LTA; septic shock; antibacterial; fungicide; virucide;
immunomodulator; anticoagulant activity;
                                                                                                                                                                                                         antimicrobial; ophthalmic; prostaglandin; hypotensive; ophthalmological; intraouclar pressure; glaucoma; ocular hypetrension; hyperaemia; irritation; inflammation; conjunctiva; ocular cell dysplasia; iridial melanocyte hyperplasia; hyperpigmentation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ophthalmic solution useful for the treatment of increased intraocular pressure comprises a prostaglandin of the F-series and an antimicrobial peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 88.4%; Score 99; DB 8; Length 18; Local Similarity 83.3%; Pred. No. 0.00023; les 15; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhesus theta-defensin-1 (RTD-1) peptide
                                                                                                                                                                Antimicrobial peptide theta-defensin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 11; 11pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ä
                             Ŕ
                          ADD35357 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADG70012 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-2003; 2003WO-US008935.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2002; 2002US-0367071P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GVCRCLCRRGVCRCLCRR
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                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CAYM-) CAYMAN CHEM CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Johnson J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-011506/01.
                                                                                                                                                                                                                                                                                                                                                                       WO2003079997-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 AA;
                                                                                                                  15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                   02-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAR-2004
                                                                      ADD35357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maxey KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADG70012;
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Best Loca Matches

RESULT 13

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MAKKE KEKAKAKE

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Gaps

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Location/Qualifiers

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The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO3523-ADO35257. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of a microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for whemolytic activity. The present sigh antimicrobial activity and low haemolytic activity. The present sequence represents the rhesus monkey wild-type theta defensin RTD-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhesus theta defensin analogue peptide aRTD-1-OH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; SEQ ID NO 1; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADO35238 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                                                   30-APR-2003; 2003US-00427715
                                                                                                                                                                                                                                                                                                                                                                                                                 30-APR-2002; 2002US-0377071P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GFCRCLCRRGVCRCICTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Selsted ME, Tran DQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-167945/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                    US2004014669-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macaca mulatta.
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                                                                                                                                                                                                                                                      22-JAN-2004
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The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO35257. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting or order of solution, as folution (e.g., contact lens solution, or eye wash colution), an inanimate object compact lens solution, or eye wash colution, an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbiscial inhibition of growth. Thus the peptides are useful as incompact in the interpolation of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents a Rhesus theta defensin analogue peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monkey, Rhesus theta defensin, RTD, antimicrobial peptide, antimicrobial, antinflammatory, antibacterial, virucide, fungicide, food, contact lans solution; eye wash solution, inflammatory response, microbicidal inhibition, microbistatic growth inhibition; disinfectant, food preservative, bacterial infection, viral infection; disinfectant, fungal infection; haemolytic activity.
                                                                                                                                                                                                                                                                                                                                                                              Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 99; DB 8; Length 18; Pred. No. 0.00023; 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhesus theta defensin analogue peptide aRTD-1-NH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; SEQ ID NO 12; 46pp; English
                                                                                        /note= "Hydroxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADO35239 standard; peptide; 18 AA
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                                                                                                                                                                                                  30-APR-2003; 2003US-00427715
                                                                                                                                                                                                                                       30-APR-2002; 2002US-0377071P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GVCRCLCRRGVCRCLCRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 83.3
Matches 15, Conservative
                                                                                                                                                                                                                                                                          (REGC ) UNIV CALIFORNIA.
               3. .16
5. .14
7. .12
                                                                                                                                                                                                                                                                                                                Selsted ME, Tran DQ
                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-167945/16.
             Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                             US2004014669-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18 AA;
                                                                      Modified-site
                                                                                                                                                              22-JAN-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             object.
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infection;

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food preservative; bacterial infection; viral fungal infection; haemolytic activity; cyclic.
                                                                                                                                                                                                                                                               (REGC ) UNIV CALIFORNIA
                                                                                                                     3. .16
5. .14
7. .12
                                                                                                                                                                                                                                                                                      Tran DQ;
                                                                                                                                                                                                                                                                                                              WPI; 2004-167945/16.
                                                                                                                                                                   US2004014669-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18 AA;
                                                                                                                               Disulfide-bond
Disulfide-bond
                                    Macaca mulatta
                                                                                                                     Disulfide-bond
                                                                                  Modified-site
                                                                                                                                                                                           22-JAN-2004.
                                                                                                                                                                                                                                                                                       Selsted ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-2004
                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AD035263;
                                                                                                                                                                                                                                                                                                                                                                         object
  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ठे
                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO3527. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or growth or survival of a microorganism in an environment such as food or obtained, an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as the repetides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensing have high antimicrobial activity and low haemolytic activity. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monkey, Rhesus theta defensin, RTD; antimicrobial peptide; antimicrobial, antilifiammatory, antibacterial; virucide; fungicide; food, contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant;
                                                                                                                                                                                                                                                                                    Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence represents a Rhesus theta defensin analogue peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.4%; Score 99; DB 8; Length 18; 83.3%; Pred. No. 0.00023; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhesus theta defensin analogue peptide RTD-5.
                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 13; 46pp; English
                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ą
                                                                                              /note= "Amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADO35256 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18
                                                                                                                                                                   30-APR-2003; 2003US-00427715.
                                                                                                                                                                                           30-APR-2002; 2002US-0377071P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GVCRCLCRRGVCRCLCRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GFCRCLCRRGVCRCICTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                (REGC ) UNIV CALIFORNIA
                                                3. .16
5. .14
7. .12
                                                                                                                                                                                                                                        Tran DQ;
                                                                                                                                                                                                                                                                WPI; 2004-167945/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                             Disulfide-bond
Disulfide-bond
Disulfide-bond
Modified-site
                                                                                                                    JS2004014669-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18 AA;
  Macaca mulatta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-2004
                                                                                                                                                                                                                                         Selsted ME,
                                                                                                                                            22-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15;
            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AD035256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                            object.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 17
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defaulted in the claims or appearing as AD035239-AD035257. The theta defaulted in the claims or appearing as AD035239-AD035257. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., context lens solution, or eye wash colution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of survival of microorganism as well as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from high annimicrobial activity and low haemolytic activity. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a theta defensin analogue defined by formulae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel theta defensin analog useful for reducing or inhibiting growth survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                    /note= "The peptide is cyclised by a covalent link between these two residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monkey RTD-1 (rhesus theta defensin 1) 2X protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 30; 46pp; English.
Location/Qualifiers
1. .18
/note= "The peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AD035263 standard; protein; 38 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-APR-2003; 2003US-00427715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-APR-2002; 2002US-0377071P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GVCRCLCRRGVCRCLC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GICRCLCRRGVCRCIC 16
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Theta defensin; antimicrobial; cyclic; bacterium; fungus; protozoan; virus; helminth; disinfectant; food preservative; analogue.

Rhesus macaque.

.2
 /note= "CNBr cleavage site"

cocation/Qualifiers

20. .21 /note= "CNBr cleavage site"

/note= "RTD-1"

.38

"RTD-1"

2. .19 /note=

WO200068265-A1

16-NOV-2000

Rhesus macaque theta defensin peptide SEQ ID NO: 8.

27-MAR-2001

AAB35037;

Ą.

AAB35037 standard; peptide; 18

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The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as AD035239-AD035257. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of the microorganism and is useful for reducing or inhibiting coupt of a microorganism in an environment such as food or food product, as colution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicadal inhibition of survival of microorganism as well as microbicadal inhibition of growth. Thus the peptides are useful as the reapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensins have they antimicrobial activity and low haemolytic activity. The present sequence is protein containing 2 copies of the rhesus monkey theta
Monkey, Rhesus theta defensin, RTD-1, antimicrobial peptide, antimicrobial, antiinflammatory, antibacterial; virucide, fungicide; food, contact lens solution, eye wash solution; inflammatory response, microbicidal inhibition, microbistatic growth inhibition; disinfectant; food preservative, bacterial infection, viral infection; disinfectant; fungal infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel theta defensin analog useful for reducing or inhibiting growth survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; Fig 17a; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-APR-2003; 2003US-00427715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-APR-2002; 2002US-0377071P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tran DQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-167945/16.
N-PSDB; ADO35262.
                                                                                                                                                                                                                                                                                                                                                                                          JS2004014669-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 38 AA;
                                                                                                                                          Macaca mulatta.
Synthetic.
                                                                                                                                                                                                 Key
Cleavage-site
                                                                                                                                                                                                                                                                                               Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Selsted ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                 22-JAN-2004
                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                     Peptide
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Anti-viral, viral infection, theta-defensin, lipid environment, amphipathic alpha-helical structure, virucide, anti-HIV, immunisation, viral growth inhibitor, viral proliferation inhibitor.
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                           Synthetic anti-viral human theta defensin peptide HTD-1 SEQ ID NO:27
                                                                        .
                                  Length 18;
                                / Match 84.8%; Score 95; DB 4; Length 18; Local Similarity 87.5%; Pred. No. 0.00062; les 14; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                          ABP53294 standard; peptide; 18 AA.
                                                                                                                                          29-JAN-2002; 2002WO-US002435
                                                                                                                   1 GVCRCLCRRGVCRCLC 16
                                                                                                                                                                                                                                                                                                                                           (first entry)
Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200260468-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                              viral growth
                                                                                                                                                                                                                                                                                                                                         13-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                  ABP53294;
                                      Query Match
                                                                            Matches
                                                                                                                                                                                                                     RESULT 20
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Novel theta defensin peptide with antimicrobial activity against bacteria, yeast, fungi, protozoa and viruses.

Example 1; Fig 2; 110pp; English

or

Ouellette AJ,

Selsted ME, Tang Y, Yuan J,

WPI; 2001-031853/04

(REGC ) UNIV CALIFORNIA

10-MAY-2000; 2000WO-US012842

99US-00309487

10-MAY-1999;

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The present invention provides theta defensin peptides and analogues which have antimicrobial activity. They can be used in the treatment of bacterial, viral, fungal, protozoan and helminthic infections, in disinfectants and as food preservatives
                                                                                                                                                                                                                                                                                                                              30-JAN-2001; 2001US-0265270P
01-AUG-2001; 2001US-0309368P
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Gaps ;

Score 99; DB 8; Length 38; Pred. No. 0.00041; Mismatches 2; Indels

88.4%; 83.3%;

Query Match

Local Similarity 83.3 les 15, Conservative

Best Loca Matches

13

1 GVCRCLCRRGVCRCLCRR 18

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2 GFCRCLCRRGVCRCICTR

RESULT 19 AAB35037

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Misc-difference 18
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Disulfide-bond 7
Misc-difference 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
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                                                           WO200285401-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE33863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                        The present invention describes a method (MI) of using a first anti-viral peptide (I) comprising a theta-defensin peptide in an amphipathic alphabatical structure in a lipide environment for reducing the infectivity of a virus. (I) can have virucide and anti-HVV activities, and can be used to reduce virus growth, infectivity burden, shed, and development of antipartial resistance. (I) can be used for inhibiting the growth and proliferation of a virus and so can be used for; (a) protecting or reating subject from a viral infection, preventing recurrent viral infection in a subject harbouring a latent virus, controlling virus in subject harbouring a latent virus, controlling virus speread within a virally-infected subject (VS), reducing virus latent virus, ontrolling virus shed from a VS, reducing percentage of VS in a population regardless of viral infection status, or inducing latency in a VS, (b) reducing the infectivity of a virus; and (c) rendering virus.

Contaminated tissue or fluid sample safe for use, or reducing the number of infections virus particles in a population of viruses. (MI) is useful for reducing the infectivity of a virus in sheep, cattle, horses, swine, cats, fowl and humans e.g. an enveloped virus infecting human such as a mannistered to a patient who is immunosuppressed or to a subject who is not infected with the virus, where the first anti-viral peptide is administered to a patient who is immunosuppressed or to a subject who is anti-viral peptide is administered prior to or subsequent to the virus contacting the subject. The anti-viral peptide is administered to a subject who is contacting the virus and human there a defensing anti-viral peptide is a human there defensing with the virus of the virus contacting the subject. The anti-viral peptide is a human there defensing anti-viral peptide is sequence represents a human there defensing anti-viral peptide is sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Retrocyclin, infection, sexually transmitted disease, gene therapy, HIV, human immunodeficiency virus, bacterial vaginosis, ophthalmic infection, antibiotic modelling, antimicrobial; human; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Linked to amino acid at position 18 to form a cyclic structure"
3. 16
7. 12
                                                                                                    New method of using a first anti-viral peptide comprising a Theta-defensin peptide in an amphipathic Alpha-helical structure in a lipid environment for reducing the infectivity of a virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                            Tack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                            PB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.1%; Score 92; DB 5; Length 18; 66.7%; Pred. No. 0.0013; ive 4; Mismatches 2; Indels
                                              Mccray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               given in the exemplification of the present invention
                                           Roller R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                            Stinski M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA.
                                                                                                                                                                 Disclosure; Page 9; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE33801 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18
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                 (IOWA ) UNIV IOWA RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GVCRCLCRRGVCRCLCRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human retrocyclin peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Conservative
                                            Stapleton J,
                                                                           WPI; 2002-674815/72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE33801;
                                           Maury W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
AAE33801
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of the invention are useful for preventing refroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin-mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is human retrocyclin peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              novel retrocyclin peptides. Peptides and methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Retrocyclin, infection, sexually transmitted disease, gene therapy, HIV, human immunodeficiency virus; bacterial vaginosis; ophthalmic infection, antibiotic modelling; antimicrobial; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Linked to amino acid at position 18 to form a structure"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
/note= "Linked to amino acid at position 1 to form a cyclic structure"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Linked to amino acid at position 1 to form a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 92; DB 6; Length 18; Pred. No. 0.0013; 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                          Hong TB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .18
'note= "D-form residues"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transmitted diseases, vaginosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; Page 24; 72pp; English
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66.7%;
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nes 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                          Lehrer RI, Waring AJ,
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Hong

Cole AM,

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The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin-mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful for modelling and screening novel sequence is human retrocyclin peptide analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 retrocyclin; cyclic; primate; retroviral infection; circular minidefensin; antibacterial; virucide; vaccine; immunotherapy; microbial; viral; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually transmitted diseases, vaginosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 24; 72pp; English.
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1 GICRCICGRGICRCICGR 18
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Best Local Similarity 66.7%;
Matches 12; Conservative
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[LEHR/) LEHRER R I.
[WARI/) WARING A J.
                                                                                                                                                                                                                                                                                     (REGC ) UNIV CALIFORNIA
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WARING A J.
COLE A M.
HONG T B.
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ADNO8176
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The invention relates to a novel isolated retrocyclin peptide. The invention further provides: a cyclic polypeptide; an isolated nucleic acid encoding a primate retrocyclin; a method for preventing retroviral infection in a cell by administering an effective dose of a circular corpusion of administering an effective dose of retrocyclin to the corpusions by administering an effective dose of retrocyclin to the microbial organisms by administering an effective dose of retrocyclin as a microbial organisms; a method for administering restrocyclin as a therapeutic agent to a patient with an established microbial or viral infection; and a method for administering retrocyclin as a prophylactic agent to prevent a microbial or viral infection in a patient at risk of developing such infection. The retrocyclin peptide can be used to treat a viral infection such as HIV-1. The retrocyclin peptide can be used to treat a viral infection and be used in immunotherapy. The peptide and polypeptides are useful as the invention. This sequence represents a retrocyclin microbial and viral infections. This sequence represents a retrocyclin cuch as the invention.
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                                                            d retrocyclin peptides and cyclic polypeptides, useful as and prophylactic agents for treating and preventing microbial
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Pred. No. 0.0013;
4; Mismatches 2; Indels
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                                                                                                                                     Claim 9; SEQ ID NO 1; 82pp; English
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66.7%;
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01-AUG-2001; 2001US-0309368P.
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Les 12, Conservative
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                                                                                   therapeutic and propl
and viral infections
              WPI; 2004-340883/31.
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                                N-PSDB; ADNO8193
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Synthetic.
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Score 92; DB 6; Length 18; Pred. No. 0.0013; 1; Mismatches 2; Indels

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(first entry)

Hong TB;

Cole AM,

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Misc-difference
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Disulfide-bond
Misc-difference
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                                                                                                      Lehrer RI,
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Matches
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                                                                The present invention describes a method (MI) of using a first anti-viral computed (I) comprising a theta-defensin peptide in an amphipathic alphace (I) computating a theta-defensin peptide in an amphipathic alphact beliated structure in a lipid environment for reducing the infectivity of a virus. (I) can have virudide and anti-HIV activities, and can be used for inhibiting the growth and confideration of a virus and so can be used for inhibiting the growth and proliferation of a virus in fection, preventing recurrent viral confection in a subject harbouring a latent virus, controlling virus in subject harbouring a latent virus, controlling virus shed from a Virally-infected subject (VS), reducing virus latent viral burden in a VS, reducing virus shed from a VS, reducing percentage of VS in a virus and contraminated tissue or fluid sample safe for use, or reducing the number of the fortious virus particles in a population of viruses. (MI) is useful for reducing the infectivity of a virus; and (c) rendering virus of infectious virus particles in a population of viruses, waine, cars, fowl and humans e.g. an enveloped virus infecting humans such as human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is administered prior to or subsequent to the virus contacting the subject. The anti-viral peptide is most preferably administered to a subject who is immunosuppressed or to a subject who is contacting the virus. The present contacting peptide is contacting the virus. The present contacting peptide is contacting peptide. Which is peptide virus in the exemplification of the present virus in the exemplification of
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3. .16
5. .14
defensin peptide in an amphipathic Alpha-helical structure in a lipid
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Pred. No. 0.0028;
3; Mismatches 3; Indels
               environment for reducing the infectivity of a virus.
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                                          Disclosure; Page 10; 65pp; English
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Best Local Similarity 66.7
Matches 12; Conservative
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Disulfide-bond 5
Disulfide-bond 7
Misc-difference 1
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Misc-difference
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AAE33804
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3. .16
5. .14
7. .12
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                                                                                                                                                                                                                                                                                              New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections of treating patients having the infections, such as HIV, sexually transmitted diseases.
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                                                                                                                                                                             Hong TB;
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/note= "D-form residues"
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18-APR-2002; 2002WO-US012353
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                                                                                                                   (REGC ) UNIV CALIFORNIA
                                                                                                                                                                             Waring AJ,
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18-APR-2001; 2001US-0284855P

(REGC ) UNIV CALIFORNIA

Hong

Cole AM,

Waring AJ,

Lehrer RI,

WPI; 2003-103387/09

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Matches
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                                                                                                                                             The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually retransmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin-mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is human retrocyclin peptide analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV; human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; cyclic.
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3. .16
5. .14
                                                                          New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually transmitted diseases, vaginosis.
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61.1%;
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GICRCICGKGICRCICGR
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Best Local Similarity 61.1.
Best Local 11; Conservative
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Disulfide-bond 5
Disulfide-bond 7
Misc-difference 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV; human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; cyclic.
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                                                     New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually
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66.7%; Pred. No. 0.0028;
ive 3; Mismatches 3; Indels
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                                                                                                                         transmitted diseases, vaginosis.
                                                                                                                                                                 Claim 9; Page 24; 72pp; English.
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Disulfide-bond 5
Disulfide-bond 7
Misc-difference 1
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Misc-difference
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                                                                           The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiancy virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin-mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is human retrocyclin peptide analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monkey, Rhesus theta defensin, RTD, antimicrobial peptide, antimicrobial, antinflammatory, antibacterial, virucide, fungicide, food, contact lens solution, eye wash solution, inflammatory response, microbicidal inhibition, microbistatic growth inhibition, disinfectant, food preservative, bacterial infection, viral infection, disinfectant, fungal infection, haemolytic activity.
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treating patients having the infections, such as HIV, sexually transmitted diseases, vaginosis.
                                                                                                                                                                                                                                                         Score 89; DB 6; Length 18;
Pred. No. 0.0028;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhesus theta defensin analogue peptide 5:3 aRTD-3-NH.
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                                              Claim 9; Page 24; 72pp; English.
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Best Local Similarity 61.1%;
Matches 11; Conservative
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Disulfide-bond
Modified-site
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                                                                                                                                                                                                                            Sequence 18 AA;
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defension analogue is useful for reducing or inhibiting growth or survival of amicroorganism in an envivionment capable of sustaining the growth or survival or survival of the microorganism and is useful for reducing or inhibiting converted to the microorganism and is useful for reducing or inhibiting prowth or survival of a microorganism in an environment such as food or food product, a solution (e.g., conteat lens solution), or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated retrocyclin peptides and cyclic polypeptides, useful as therapeutic and prophylactic agents for treating and preventing microbial and viral infections.
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circular minidefensin, antibacterial, virucide, vaccine, immunotherapy;
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WARING A J.
COLE A M.
HONG T B.
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                                                                                                                                                                                                                                                                                    Sequence 18 AA;
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Matches
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organisms by administering an effective dose of retrocyclin to the microbial organisms; a method for administering restrocyclin as a therapeutic agent to a patient with an established microbial or viral infection; and a method for administering retrocyclin as a prophylactic agent to prevent a microbial or viral infection in a patient at risk of developing such infection. The retrocyclin peptide has antibacterial and virucide activities. The retrocyclin peptide can be used to treat a viral infection such as HIV-1. The retrocyclin peptide can be used as a vaccine and can be used in immnotherapy. The peptide and polypeptides are useful as therapeutic and prophylactic agents for treating and preventing microbial and viral infections. This sequence represents a retrocyclin
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circular minidefensin; antibacterial; virucide; vaccine; immunotherapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADNO8179 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human retrocyclin peptide, RC-103
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                                                                                                                                                                                                                                                                                  Local Similarity 61.1
es 11; Conservative
                                                                                                                                                                                              peptide of the invention
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WARING A J.
COLE A M.
HONG T B.
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                                                                                                                                                                                                                                   Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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(LEHR/) I
(WARI/) V
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Matches
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infection, and a method for administering retrocyclin as a prophylactic agent to prevent a microbial or viral infection in a patient at risk of developing such infection. The retrocyclin peptide has antibacterial and virucide activities. The retrocyclin peptide can be used to treat a viral infection such as HIV-1. The retrocyclin peptide can be used as a vaccine and can be used in immunotherapy. The peptide and polypeptides are useful as therapeutic and prophylactic agents for treating and preventing microbial and viral infections. This sequence represents a retrocyclin peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rrocyclin peptides and cyclic polypeptides, useful as prophylactic agents for treating and preventing microbial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   retrocyclin, cyclic; primate; retroviral infection; circular minidefensin; antibacterial; virucide; vaccine; immunotherapy;
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                                                                                                                                                                                                          79.5%; Score 89; DB 8; Length 18; 66.7%; Pred. No. 0.0028; ive 3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                    ADN08178 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human retrocyclin peptide, RC-102
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LEHRER R I.
WARING A J.
COLE A M.
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and viral infections.
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                                                                                                                                                                               Sequence 18 AA;
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retrocyclin peptide analogue

sequence is human

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Query Match
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virucide activities. The retrocyclin peptide can be used to treat a viral infection such as HIV-1. The retrocyclin peptide can be used as a vaccine and can be used in immunotherapy. The peptide and polypeptides are useful as therapeutic and prophylactic agents for treating and preventing microbial and viral infections. This sequence represents a retrocyclin peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or trating patients having infections such as HIV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin-mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy. The present
                                                                                                                                                                                                                                                                                                                        Retrocyclin, infection, sexually transmitted disease, gene therapy, HIV, human immunodeficiency virus, bacterial vaginosis, ophthalmic infection, antibiotic modelling; antimicrobial; cyclic.
                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually transmitted diseases, vaginosis.
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3. .16
5. .14
7. .12
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                                                                                                  Query Match 79.5%; Score 89; DB 8; Length 18; Best Local Similarity 66.7%; Pred. No. 0.0028; Matches 12; Conservative 3; Mismatches 3; Indels
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Disulfide-bond 5
Disulfide-bond 7
Misc-difference 1
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Misc-difference
                                                                                Seguence 18 AA
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                                                                                                                                                                                                                                                                                                                                                                     Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Retrocyclin, infection, sexually transmitted disease, gene therapy, HIV, human immunodeficiency virus, bacterial vaginosis, ophthalmic infection, antibiotic modelling, antimicrobial, cyclic.
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                                          Score 88; DB 6; Length 18; Pred, No. 0.0035;
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                                                                                                                                      1 GVCRCLCRRGVCRCLCRR 18
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                                                                                                                                                                                                                                                                                                      AAE33806 standard; peptide; 18
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                                       Match 78.6%;
Local Similarity 66.7%;
hes 12; Conservative
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Disulfide-bond 5
Disulfide-bond 7
Misc-difference 1
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Misc-difference
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  Sequence 18
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                                            Query Match
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Length 18;

DB 6;

78.6%; Score 88;

Matches

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RESULT 35 ADN08180

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1 GVCRCLCRRGVCRCLCRR 18
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                                                                                                                                                                                                                                                                                                       retrocyclin, cyclic, primate, retroviral infection;
circular minidefensin; antibacterial; virucide; vaccine; immunotherapy;
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                             Indels
Pred. No. 0.0035;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; SEQ ID NO 5; 82pp; English.
                                                                                                                                                                                                                                                                         Human retrocyclin peptide, RC-104.
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                                                                                ADN08180 standard; peptide; 18
                                                             1 GVCRCLCRRGVCRCLCRR 18
             66.7%;
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LEHR/) LEHRER R I.
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WARING A J.
COLE A M.
HONG T B.
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               Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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The invention relates to a novel isolated retrocyclin peptide. The invention further provides: a cyclic polypeptide, an isolated nucleic caid encoding a primate retrocyclin, a method for preventing retroviral infection in a cell by administering an effective dose of a circular corpanisms by administering an effective dose of retrocyclin to the cell, a method for killing microbial corpanisms, a method for administering restrocyclin to the microbial organisms, a method for administering restrocyclin as a cell infection, and a method for administering retrocyclin as a prophylactic agent to prevent a microbial or viral infection; and a method for administering retrocyclin as a prophylactic corpulation of the retrocyclin peptide has antibacterial and ceveloping such infection. The retrocyclin peptide can be used to treat a viral infection such as HIV-1. The retrocyclin peptide can be used as a vaccine cond can be used in immunotherapy. The peptide can be used as a vaccine and can be used in immunotherapy. The peptide and polypeptides are useful as therapeutic and prophylactic agents for treating and preventing microbial and viral infections. This sequence represents a retrocyclin peptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   retrocyclin; cyclic; primate; retroviral infection;
circular minidefensin; antibacterial; virucide; vaccine; immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; SEQ ID NO 6; 82pp; English.
                                                                                                                                                                                                                                    ADN08181 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human retrocyclin peptide, RC-105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cole AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GICRCICGRGYCRCICGR 18
1 GYCRCICGRGICRCICGR 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAY-2003; 2003WO-US014106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAY-2002; 2002US-00141645
                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   microbial; viral; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lehrer RI, Waring AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LEHR/) LEHRER R I.
(WARI/) WARING A J.
(COLE/) COLE A M.
(HONG/) HONG T B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-340883/31.
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B;

RESULT 37 AAB35046

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The present invention describes a method (M1) of using a first anti-viral peptide (I) comprising a theta-defensin peptide in an amphipathic alphace peptide (I) comprising a theta-defensin peptide in an amphipathic alphace helical structure in a lipid environment for reducing the infectivity of a virus. (I) can have virucide and anti-HIV activities, and can be used for interaction of a virus and so can be used for inhibiting the growth and conce virus and so can be used for; (a) protecting or treating subject from a viral infection, preventing recurrent viral infection in a subject harbouring a latent virus, controlling virus infection in a virally-infected subject (VS), reducing virus band from a VS, reducing virus shed from a VS, reducing virus latency in a CS; (b) reducing the infectivity of a virus; and (c) rendering virus of virus and virus; and (c) rendering virus expendation regardless of viral infection status, or inducing latency in a CS; (b) reducing the infectivity of a virus; and (c) rendering virus of infectious virus particles in a population of viruses. (MI) is useful to rear four and humans e.g. an enveloped virus infecting humans such as human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is administered prior to or subsequent to the virus contacting the subject. The anti-viral peptide is most preferably administered to a patient where the first anti-viral peptide is a most preferably administered to a patient where the first anti-viral peptide is corrunically, latently or acutely infected with the virus. The present sequence represents a rhesus monkey thete defensin anti-viral peptide, which is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV; human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; cyclic.
                                                                                                                                                                                                                                           New method of using a first anti-viral peptide comprising a Theta-defensin peptide in an amphipathic Alpha-helical structure in a lipid environment for reducing the infectivity of a virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Linked to amino acid at position 18 to form a
                                                                                                                                                         Tack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 76.8%; Score 86; DB 5; Length 18; Best Local Similarity 66.7%; Pred. No. 0.0058; Matches 12; Conservative 2; Mismatches 4; Indels
                                                                                                                                                         Mccray PB,
                                                                                                                                                         Roller R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RC-101/103 retrocyclin peptide analogue.
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1
                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 10; 65pp; English.
                                                                                                                                                         Stinski M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ą.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE33865 standard; peptide; 18
29-JAN-2002; 2002WO-US002435.
                                           30-JAN-2001; 2001US-0265270P.
01-AUG-2001; 2001US-0309368P.
                                                                                                             (IOWA ) UNIV IOWA RES FOUND
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                                                                                                                                                           Stapleton J,
                                                                                                                                                                                                       WPI; 2002-674815/72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
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                                                                                                                                                           Maury W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides theta defensin peptides and analogues which have antimicrobial activity. They can be used in the treatment of bacterial, viral, fungal, protozoan and helminthic infections, in disinfectants and as food preservatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-viral, viral infection, theta-defensin, lipid environment, amphipathic alpha-helical structure, virucide, anti-HIV, immunisation, viral growth inhibitor, viral proliferation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                         cyclic; bacterium; fungus; protozoan; food preservative; analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel theta defensin peptide with antimicrobial activity against bacteria, yeast, fungi, protozoa and viruses.
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Pred. No. 0.0058;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-viral theta defensin peptide RTD-2 SEQ ID NO:28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouellette AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP53295 standard; peptide; 18 AA.
                                                                                         AAB35046 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 15; Fig 16; 110pp; English.
                                                                                                                                                                                                                                                                           Theta defensin; antimicrobial; virus; helminth; disinfectant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GVCRCLCRRGVCRCLCRR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang Y, Yuan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-MAY-2000; 2000WO-US012842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-00309487.
                                                                                                                                                                                                                                  Theta defensin SEQ ID NO: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 66.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GFCRCICTRGFCRCICTR
                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200260468-A2.
                                                                                                                                                                                                                                                                                                                                                                                             WO200068265-A1.
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                                                                                                                                                                                                                                                                                                                                               Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Selsted ME,
                                                                                                                                                                                   27-MAR-2001
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                                                                                                                                        AAB35046;
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Gaps

RESULT 38 ABP53295

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Monkey, Rhesus theta defensin, RTD-2, antimicrobial peptide, cyclic, antimicrobial, antiinflammatory, antibacterial, virucide, fungicide, food; contact lens solution; eye wash solution; inflammatory response, microbicidal inhibition, microbistatic growth inhibition; disinfectant; food preservative, bacterial infection; viral infection; disinfectant; fungal infection; haemolytic activity.

    18 / Increament of the period of the control of the c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-103387/09
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                                                                                                                                                                                                                                       WO200285401-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .5-JUL-2004
                                                                                                                                                                                                                                                                                                    31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lehrer RI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AD035230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually transmitted diseases, vaginosis.
                                                                                                                                                /note= "Linked to amino acid at position 1 to form cyclic structure"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 24; 72pp; English.
            structure"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cole AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GVCRCLCRRGVCRCLCRR 18
                                                                                                                                                                                                                                                                                                                                                              18-APR-2002; 2002WO-US012353.
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Best Local Similarity 61.1%;
Matches 11; Conservative
cyclic & 3. .16 5. .14 7. .12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waring AJ,
                                  Disulfide-bond 3. . Disulfide-bond 5. . Disulfide-bond 7. . Misc-difference 18
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Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate

WPI; 2004-167945/16.

Selsted ME,

30-APR-2003; 2003US-00427715 30-APR-2002; 2002US-0377071P (REGC ) UNIV CALIFORNIA

1.4

US2004014669-A1 Disulfide-bond Disulfide-bond

22-JAN-2004.

Example 1; SEQ ID NO 2; 46pp; English

object.

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The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO3527. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of a microorganism in an environment such as food or growth or survival of a microorganism in an environment such as food or or solution, an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbistatic inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as the repetides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensing have bacterial, viral, fungal or other infection. The theta defensing have been antimicrobial activity and low haemolytic activity. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nign antimicrobial activity and low haemolytic activity. The present sequence represents the rhesus monkey wild-type theta defensin RTD-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 AA;
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Gaps ö Match 76.8%; Score 86; DB 8; Length 18; Local Similarity 66.7%; Pred. No. 0.0058; les 12; Conservative 2; Mismatches 4; Indels 1 GFCRCICTRGFCRCICTR 18 1 GVCRCLCRRGVCRCLCRR 18 Best Loca Matches 8

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Search completed: October 26, 2004, 15:34:54 Job time : 115 secs

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